

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2004, 08:17:56 ; Search time 1513 Seconds

(Without alignments)  
7516.772 Million cell updates/sec

Title: US-09-675-650-2

Perfect score: 278

Sequence: 1 caggaagcacaagaagc.....ggtccacaagacatgcaac 278

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapept 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: gb\_ba:\*
- 2: gb\_htg:\*
- 3: gb\_in:\*
- 4: gb\_om:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_sts:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vi:\*
- 15: em\_ba:\*
- 16: em\_fun:\*
- 17: em\_hum:\*
- 18: em\_in:\*
- 19: em\_mu:\*
- 20: em\_om:\*
- 21: em\_or:\*
- 22: em\_ov:\*
- 23: em\_pat:\*
- 24: em\_ph:\*
- 25: em\_pl:\*
- 26: em\_ro:\*
- 27: em\_sts:\*
- 28: em\_un:\*
- 29: em\_vi:\*
- 30: em\_htg\_hum:\*
- 31: em\_htg\_inv:\*
- 32: em\_htg\_other:\*
- 33: em\_htg\_mus:\*
- 34: em\_htg\_pln:\*
- 35: em\_htg\_rtd:\*
- 36: em\_htg\_mam:\*
- 37: em\_htg\_vrt:\*
- 38: em\_sy:\*
- 39: em\_htgo\_hum:\*
- 40: em\_htgo\_mus:\*
- 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 278   | 100.0       | 278    | 6     | AX107858    |
| 2          | 266   | 95.7        | 812    | 6     | AX261039    |
| 3          | 266   | 95.7        | 812    | 6     | AR278570    |
| 4          | 266   | 95.7        | 812    | 6     | AX106207    |
| 5          | 266   | 95.7        | 812    | 6     | AX106690    |
| 6          | 266   | 95.7        | 812    | 6     | AX140981    |
| 7          | 266   | 95.7        | 812    | 6     | AX200841    |
| 8          | 266   | 95.7        | 812    | 6     | AX267497    |
| 9          | 266   | 95.7        | 812    | 6     | BD082484    |
| 10         | 266   | 95.7        | 1872   | 6     | BD082483    |
| 11         | 266   | 95.7        | 2037   | 6     | BD082482    |
| 12         | 266   | 95.7        | 2229   | 6     | AR261037    |
| 13         | 266   | 95.7        | 2229   | 6     | AR278568    |
| 14         | 266   | 95.7        | 2229   | 6     | AX106205    |
| 15         | 266   | 95.7        | 2229   | 6     | AX106688    |
| 16         | 266   | 95.7        | 2229   | 6     | AX140979    |
| 17         | 266   | 95.7        | 2229   | 6     | AX200839    |
| 18         | 266   | 95.7        | 2229   | 6     | AX267495    |
| 19         | 266   | 95.7        | 2426   | 6     | AR261038    |
| 20         | 266   | 95.7        | 2426   | 6     | AR278569    |
| 21         | 266   | 95.7        | 2426   | 6     | AX106206    |
| 22         | 266   | 95.7        | 2426   | 6     | AX106689    |
| 23         | 266   | 95.7        | 2426   | 6     | AX140980    |
| 24         | 266   | 95.7        | 2426   | 6     | AX200840    |
| 25         | 266   | 95.7        | 2426   | 6     | AX267496    |
| 26         | 266   | 95.7        | 3112   | 6     | AR261036    |
| 27         | 266   | 95.7        | 3112   | 6     | AR278567    |
| 28         | 266   | 95.7        | 3112   | 6     | AX106204    |
| 29         | 266   | 95.7        | 3112   | 6     | AX140978    |
| 30         | 266   | 95.7        | 3112   | 6     | AX200838    |
| 31         | 266   | 95.7        | 3112   | 6     | AX267494    |
| 32         | 266   | 95.7        | 3112   | 6     | BD082485    |
| 33         | 266   | 95.7        | 3112   | 6     | AR261166    |
| 34         | 266   | 95.7        | 3112   | 6     | AR278697    |
| 35         | 266   | 95.7        | 3112   | 6     | AX200988    |
| 36         | 266   | 95.7        | 3112   | 6     | AX267716    |
| 37         | 266   | 95.7        | 3112   | 6     | AF103907    |
| 38         | 266   | 95.7        | 3112   | 6     | AX107857    |
| 39         | 266   | 95.7        | 3112   | 6     | AF103908    |
| 40         | 266   | 95.7        | 3112   | 6     | AL359314    |
| 41         | 266   | 95.7        | 3112   | 6     | AR237401    |
| 42         | 266   | 95.7        | 3112   | 6     | AR260894    |
| 43         | 266   | 95.7        | 3112   | 6     | AR278425    |
| 44         | 266   | 95.7        | 3112   | 6     | AX106203    |
| 45         | 266   | 95.7        | 3112   | 6     | AX106203    |

## ALIGNMENTS

| RESULT 1 | LOCUS    | DEFINITION                        | ACCESSION | VERSION    | KEYWORDS    | SOURCE | ORGANISM  | REFERENCE | AUTHORS                              | TITLE   | JOURNAL                             |
|----------|----------|-----------------------------------|-----------|------------|-------------|--------|---|-----------|--------------------------------------|---|-------------------------------------|
| AX107858 | AX107858 | Sequence 2 from Patent WO0133550. | AX107858  | AX107858.1 | GI:13923250 |        | Homo sapiens (human)  | 1         | Busse, U., Chypre, C. and Fradet, Y. | Pca3 messenger rna species in benign and malignant prostate tissues | Patent: WO 0133550-A 2 05-APR-2001; |
|          |          |                                   |           |            |             |        | Homo sapiens  |           |                                      |   |                                     |
|          |          |                                   |           |            |             |        | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |           |                                      |   |                                     |
|          |          |                                   |           |            |             |        | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.         |           |                                      |   |                                     |

| Diagnocure Inc. (CA)  |                 |   |                                      |             |  |  |  |  |  |
|-----------------------|-----------------|---|--------------------------------------|-------------|--|--|--|--|--|
| FEATURES              | Source          | Location/Qualifiers                                       |                                      |             |  |  |  |  |  |
|                       |                 | 1..278  |                                      |             |  |  |  |  |  |
|                       |                 | /organism="Homo sapiens"                                  |                                      |             |  |  |  |  |  |
|                       |                 | /mol_type="genomic DNA"                                   |                                      |             |  |  |  |  |  |
|                       |                 | /db_xref="taxon:9606"                                     |                                      |             |  |  |  |  |  |
| BASE COUNT            | 90 a            | 54 c  | 75 g                                 | 59 t        |  |  |  |  |  |
| ORIGIN                |                 |   |                                      |             |  |  |  |  |  |
| Query Match           | 100.0%          | Score 278;  | DB 6;                                | Length 278; |  |  |  |  |  |
| Best Local Similarity | 100.0%;         | Pred. No. 4.6e-72;  |                                      |             |  |  |  |  |  |
| Matches 278;          | Conservative 0; | Mismatches 0;   | Indels 0;                            | Gaps 0;     |  |  |  |  |  |
| QY                    | 1               | CAGGAGACAAAAGGAAGCA                                       | CAGAGATCCCTGGGAGAAATGCCCGCGGCATCTGGG | 60          |  |  |  |  |  |
|                       |                 |   |                                      |             |  |  |  |  |  |
| DB                    | 1               | CAGGAAGACAAAAGGAAGCA                                      | CAGAGATCCCTGGGAGAAATGCCCGCGGCATCTGGG | 60          |  |  |  |  |  |
| QY                    | 61              | TCATCGATGACCTTCGCCCTGTGCTTCGCCGCTTGGAGGGAAGACATTAGAAATG   | 120                                  |             |  |  |  |  |  |
|                       |                 |   |                                      |             |  |  |  |  |  |
| DB                    | 61              | TCATCGATGAGACCTTCGCCCTGTGCTTCGCCGCTTGGAGGGAAGACATTAGAAATG | 120                                  |             |  |  |  |  |  |
| QY                    | 121             | AATTGATGTCTCTTAAAGATGGGCA                                 | GAAAAAGATCCTGTTGTGATATTATTG          | 180         |  |  |  |  |  |
|                       |                 |   |                                      |             |  |  |  |  |  |
| DB                    | 121             | AATTGATGTCTCTTAAAGATGGGCA                                 | GAAAAAGATCCTGTTGTGATATTATTG          | 180         |  |  |  |  |  |
| QY                    | 181             | AACGGATTACAGATTTGAATGAAGTAC                               | CAAAATGACATTCACCATGAGAGAAAC          | 240         |  |  |  |  |  |
|                       |                 |   |                                      |             |  |  |  |  |  |
| DB                    | 181             | AACGGATTACAGATTTGAATGAAGTAC                               | CAAAATGACATTCACCATGAGAGAAAC          | 240         |  |  |  |  |  |
| QY                    | 241             | AGACGAGAAATCTTGATGGCTTCA                                  | CAAGACATGCAAC                        | 278         |  |  |  |  |  |
|                       |                 |   |                                      |             |  |  |  |  |  |
| DB                    | 241             | AGACGAGAAATCTTGATGGCTTCA                                  | CAAGACATGCAAC                        | 278         |  |  |  |  |  |

| LOCUS                 | AR261039  | 812 bp   | DNA         | linear      | PAT 29-JAN-2003 |
|-----------------------|---|--|-------------|-------------|-----------------|
| DEFINITION            | Sequence  | 471  | from patent | US 6321716. |                 |
| ACCESSION             | AR261039  |  |             |             |                 |
| VERSION               | AR261039.1  | GI:28071802  |             |             |                 |
| KEYWORDS              |   |  |             |             |                 |
| SOURCE                | Unknown.  |  |             |             |                 |
| ORGANISM              | Unknown.  |  |             |             |                 |
| REFERENCE             | Unclassified.   |  |             |             |                 |
| AUTHORS               | 1 (bases 1 to 812)  |  |             |             |                 |
| TITLE                 | Mashiki, Z. and Harada, J.  |  |             |             |                 |
| JOURNAL               | Negative pressure control apparatus for engine mounted in vehicle |  |             |             |                 |
| FEATURES              | Patent: US 6321716-A 471 27-NOV-2001;                             |  |             |             |                 |
|                       | Location/Qualifiers   |  |             |             |                 |
|                       | 1..812  |  |             |             |                 |
|                       | /organism="unknown"   |  |             |             |                 |
| BASE COUNT            | 198 a   | 189 c  | 169 g       | 256 t       |                 |
| ORIGIN                |   |  |             |             |                 |
| Query Match           | 95.7%;  | Score 266;   | DB 6;       | Length 812; |                 |
| Best Local Similarity | 99.6%;  | Pred. NO. 2e-66;   |             |             |                 |
| Matches 277;          | Conservative 0;   | Mismatches 0;  | Indels 1;   | Gaps 1;     |                 |
| QY                    | 1   | CAGGAGACAAAAGGAGGACACAGGATCCCTGGGAGAAATGCCGCGCCGCATCTTGGG  | 60          |             |                 |
| DB                    | 562   | CAGGAGACAAAAGGAGGACACAGGATCCCTGGGAGAAATGCCGCGCCGCATCTTGGG  | 503         |             |                 |
| QY                    | 61  | TCATCGATGAGCCTCGCCCTGTGCTGCTGCTCCGCTTGTGAGGAGAGCATTAGAAATG | 120         |             |                 |
| DB                    | 502   | TCATCGATGAGCCTCGCCCTGTGCTGCTGCTCCGCTTGTGAGGAGAGCATTAGAAATG | 443         |             |                 |
| QY                    | 121   | AATTGATGTGTTCTCTTAAGATGGGACGAGAAACAGATCCTGTGTGGATATTATTG   | 180         |             |                 |
| DB                    | 442   | AATTGATGTGTTCTCTTAAGATGGGACGAGAAACAGATCCTGTGTGGATATTATTG   | 383         |             |                 |
| QY                    | 181   | AACGGGATTACGATTTGAATGAAGTCAACCAAAAGTGACATTACCAATGAGAGAAAC  | 240         |             |                 |
| DB                    | 382   | AACGGGATTACGATTTGAATGAAGTCAACCAATGAGAGAAAC                 | 324         |             |                 |

| Query Match           | 95.7%        | Score 266       | DB 6         | Length 812        |
|-----------------------|--------------|-----------------|--------------|-------------------|
| Best Local Similarity | 99.6%        | Pred. No. 2e-68 |              |                   |
| Matches 277           | Conservative | 0               | Mismatches 0 | Indels 1; Gaps 1; |

| FEATURES   | Source  |
|------------|---|
| Db         | 562 CAGGAACCAAAAAGAGACACAGAGATCCCTGGGAAATGCGCCGCCCATCTTGGG 503    |
| Oy         | 61 TCATGATGAGCCTCGCCCTGTGCTTGTGTCGCCCTTGTGAGGAGAGACATTGAAATG 120  |
| Db         | 502 TCATCGATGAGCCCTCGCCCTGTGCTTGTGCTGCTTGTGAGGAGAGACATTGAAATG 443 |
| Oy         | 121 AATTGATGATCTCCTTAAAGATGGGAGGAAAAACAATCCTGTGTGATATTATTG 180    |
| Db         | 442 AATTGATGTGTTCTTAAAGATGGGAGGAAAAACAGATCCTGTTGTGATATTATTG 383   |
| Oy         | 181 AACGGATTACAGATTTGAATGAAGTCAACCAAGTGAATTAACAATGAGAGAAAC 240    |
| Db         | 382 AACGGATTACAGATTTGAATGAAGTCA CAAGTGAATTAACAATGAGAGAAAC 324     |
| Oy         | 241 AGACGAGAAAAATCTTGATGCTTACACAAACATGCAAC 278                    |
| Db         | 323 AGACGAGAAAAATCTTGATGCTTACACAAACATGCAAC 286                    |
| RESULT 4   |   |
| LOCUS      | AX106207/c 812 bp DNA linear PAT 30-APR-2001                      |
| DEFINITION | Sequence 345 from Patent WO0125273.                               |
| ACCESSION  | AX106207  |
| VERSION    | AX106207.1 GI:13921896  |
| KEYWORDS   |   |
| SOURCE     | Homo sapiens (human)  |
| ORGANISM   | Homo sapiens  |
| REFERENCE  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| AUTHORS    | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.         |
| TITLE      | Skely, Y.A., Xu, J., Cheever, M.A. and Reed, S.G.                 |
| JOURNAL    | Compositions and methods for wli specific immunotherapy           |
|            | Patent: WO 0125273-A 345 12-APR-2001;                             |
|            | CORIXA CORPORATION (US)   |
|            | Location/Qualifiers   |
|            | 1..812  |



**TITLE** Reed, S.G., Kalos, M.D., Fanger, G.R., Day, C.H., Retter, M.W., Stolk, J.A., Skeiky, Y.A., Wang, A. and Meagher, M.J.  
Compositions and methods for the therapy and diagnosis of prostate cancer  
**JOURNAL** Patent: WO 0151633-A 471 19-UU-2001; CORIXA CORPORATION (US)

| source  | location/qualifiers |
|---------|---------------------|
| 1. .812 |                     |

| BASE COUNT | 198 a | 189 c | 169 g | 256 t |
|------------|-------|-------|-------|-------|
| ORIGIN     |       |       |       |       |

|                       |              |                  |            |             |
|-----------------------|--------------|------------------|------------|-------------|
| Query Match           | 95.7%;       | Score 266;       | DB 6;      | Length 812; |
| Best Local Similarity | 99.6%;       | Pred. No. 2e-68; |            |             |
| Matches 277;          | Conservative | 0;               | Mismatches | 0;          |
|                       |              |                  | Indels     | 1;          |
|                       |              |                  | Gaps       | 1.          |

| QY | 1   | CAGGAAGCACA   | AAAGGAGAC      | CAGAGATCC       | CTGGAGAAATG           | CCGCGCGCATCTTGGG | 60  |
|----|-----|---|----------------|-----------------|-----------------------|------------------|-----|
| QY | 562 | CAGGAAGCACA <th>AAAGGAGAC</th> <td>CAGAGATCC</td> <td>CTGGAGAAATG</td> <td>CCGCGCGCATCTTGGG</td> <td>503</td> | AAAGGAGAC      | CAGAGATCC       | CTGGAGAAATG           | CCGCGCGCATCTTGGG | 503 |
| Db | 61  | TCATCGATGAG   | CGCTCGCCTCTG   | TGCTGTGCCGCTT   | GTGAGGAAAGCATTAGAAATG |                  | 120 |
| QY | 502 | TCATCGATGAG   | CGCTCGCCTCTG   | TGCTGTGCCGCTT   | GTGAGGAAAGCATTAGAAATG |                  | 443 |
| Db | 121 | AATTGATGTGCT  | TCTTAAAGGATGGG | CAGAGAAACAGATCC | GTGTGGGATATTATTG      |                  | 180 |
| QY | 442 | AATTGATGTGCT  | TCTTAAAGGATGGG | CAGAGAAACAGATCC | GTGTGGGATATTATTG      |                  | 383 |
| Db | 181 | AACGGGATTAC   | AGATTGGAATGAA  | TGAACTC         | CAAATGAGCATTTAC       | TGAGAGAAAC       | 240 |
| QY | 382 | AACGGGATTAC   | AGATTGGAATGAA  | TGAACTC         | CAAATGAGCATTTAC       | TGAGAGAAAC       | 324 |
| Db | 241 | AGACGAGAAAA   | TCTTGATGCTTCA  | CAACAACATGCAAC  |                       |                  | 278 |
| QY | 323 | AGACGAGAAAA   | TCTTGATGCTTCA  | CAACAACATGCAAC  |                       |                  | 286 |

|            |                                     |             |                 |
|------------|-------------------------------------|-------------|-----------------|
| RESULT 8   |                                     |             |                 |
| AX267497/c |                                     |             |                 |
| LOCUS      | AX267497                            | 812 bp      | DNA             |
| DEFINITION | Sequence 471 from Patent WO0173032. |             | linear          |
| ACCESSION  | AX267497                            |             |                 |
| VERSION    | AX267497.1                          | GI:16516261 |                 |
|            |                                     |             | PAT 26-OCT-2001 |

| REFERENCE | AUTHORS  | TITLE  |
|-----------|--|--|
| 1         | Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Rettee, M.W., Stolk, J.A., Day, C.H., Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skelky, Y.A., Hepler, W.T and Henderson, R.A. | Compositions and methods for the therapy and diagnosis of prostate |

| FEATURES | Location/Qualifiers |
|----------|---------------------|
| source   | 1. .812             |

|            |       |       |       |       |
|------------|-------|-------|-------|-------|
| BASE COUNT | 198 a | 189 c | 169 g | 256 t |
| ORIGIN     |       |       |       |       |

|                       |              |                 |            |            |
|-----------------------|--------------|-----------------|------------|------------|
| Query Match           | 95.7%        | Score 266       | DB 6       | Length 812 |
| Best Local Similarity | 99.6%        | Pred. No. 2e-68 |            |            |
| Matches 277           | Conservative | 0               | Mismatches | 0          |
|                       |              |                 | Indels     | 1          |
|                       |              |                 | Gaps       | 1          |

  

|    |   |   |    |
|----|---|---|----|
| QY | 1 | CAGGAGCACAAGAGGACACAGAGATCTCTGGAGAAATGCCCGCCCATCTTGGG | 60 |
|    |   |   |    |

|            |     |  |     |
|------------|-----|--|-----|
| D <b>b</b> | 562 | CAGGAAGCAGAAAAGAAAGACAGAGATCCCTGGGAGAAATGCCGGCGGCATCTTGGG      | 503 |
| O <b>y</b> | 61  | TCATCGATTGAGCCTTCGCCCTGTGCTGCTGTCCCCCTTTGTGAGGAAAGCATTTAAAAATG | 120 |
| D <b>b</b> | 502 | TCATCGATTGAGCCCTCGGCCCTGTGCTGTGTCCCCTTTGTGAGGAAAGCATTTAAAAATG  | 443 |
| O <b>y</b> | 121 | AATTGATGTGTTCCCTTAAGAGATGGGACGAGAAAACAGATCCCTGTTGTGATATTATTTTG | 180 |
| D <b>b</b> | 442 | AATTGATGTGTTCCCTTAAGAGATGGGACGAGAAAACAGATCCCTGTTGTGATATTATTTTG | 383 |
| O <b>y</b> | 181 | AACGGGATTACAGATTGGAATGAATGATCCAAAGTAGCATTTGCCAATGAGAGAAAAAC    | 240 |
| D <b>b</b> | 382 | AACCGGATTACAGATTGGAATGAATGATCA-CMAAGTAGCATTTGCCAATGAGAGAAAAAC  | 324 |
| O <b>y</b> | 241 | AGACGAGAAAAATCTTGATGCGCTTACACAAGACATGCAAC                      | 278 |
| D <b>b</b> | 323 | AGACGAGAAAAATCTTGATGCGCTTACACAAGACATGCAAC                      | 286 |

|            |  |             |        |     |        |                 |
|------------|--|-------------|--------|-----|--------|-----------------|
| RESULT 9   | BD082484                               | BD082484    | 820 bp | DNA | linear | PAT 27-AUG-2002 |
| LOCUS      | BD082484                               |             |        |     |        |                 |
| DEFINITION | PCA3, PCA3 genes, and methods of use.  |             |        |     |        |                 |
| ACCESSION  | BD082484                               |             |        |     |        |                 |
| VERSION    | BD082484.1                             | GI:22628094 |        |     |        |                 |
| KEYWORDS   | JP 2001522240-A/3.                     |             |        |     |        |                 |
| SOURCE     | Mastadenovirus                         |             |        |     |        |                 |
| ORGANISM   | Mastadenovirus                         |             |        |     |        |                 |
| REFERENCE  | 1 (bases 1 to 820)                     |             |        |     |        |                 |
| AUTHORS    | Bussemakers, M.J.G.                    |             |        |     |        |                 |
| TITLE      | PCA3, PCA3 genes, and methods of use   |             |        |     |        |                 |
| JOURNAL    | Patent: JP 2001522240-A 3 13-NOV-2001; |             |        |     |        |                 |

| FEATURES | Location/Qualifiers |
|----------|---------------------|
| source   | 1. .820             |

|                           |     |   |       |   |                  |       |             |            |
|---------------------------|-----|---|-------|---|------------------|-------|-------------|------------|
| BASE COUNT                | 262 | a | 169   | c | 191              | g     | 198         | t          |
| ORIGIN                    |     |   |       |   |                  |       |             |            |
| Query Match               |     |   | 95.7% |   | Score 266;       | DB 6; | Length 820; |            |
| Best Local Similarity     |     |   | 99.6% |   | Pred. No. 2e-68; |       |             |            |
| Matches 277; conservative |     |   | 0;    |   | Mismatches       | 0;    | Indels      | 1; Gaps 1; |

|    |     |   |     |
|----|-----|---|-----|
| QY | 1   | CAGGAAGCACAAGGAAGCACAAGATCCCTGGAGAAATGCCGCGCCATCTTGGG   | 60  |
| Db | 256 | CAGGAAGCACAAGGAAGCACAAGATCCCTGGAGAAATGCCGCGCCATCTTGGG   | 315 |
| QY | 61  | TCATCGATGAGCCTCGCCCTGCTGGTCCCGCTTGAGGAGACATTAGAAATG     | 120 |
| Db | 316 | TCATCGATGAGACCTCGCCCTGCTGGTCCCGCTTGAGGAGAGACATTAGAAATG  | 375 |
| QY | 121 | AATTGATGTGTTCTTAAAGATGGCAGAAAACAGATCCTGTTGGATATTATTG    | 180 |
| Db | 376 | AATTGATGTGTTCTTAAAGATGGCAGAAAACAGATCCTGTTGGATATTATTG    | 435 |
| QY | 181 | AACGGGATTACAGATTGAAATGAAGTCAACCAAGTGAATTCACATGAGAGGAAAC | 240 |
| Db | 436 | AACGGGATTACAGATTGAAATGAAGTCAACCAAGTGAATTCACATGAGAGGAAAC | 494 |

|    |     |             |             |            |            |            |          |         |     |
|----|-----|-------------|-------------|------------|------------|------------|----------|---------|-----|
| QY | 1   | CAGGAAGCACA | AAAGGAAGCA  | CACAAGAT   | CTCTGGAGAA | AAATGCCGCG | CGGCATCT | GGG     | 60  |
| Db | 256 | CAGGAAGCACA | AAAGGAAGCA  | CACAAGAT   | CTCTGGAGAA | AAATGCCGCG | CGGCATCT | GGG     | 315 |
| QY | 61  | TCATCGATGAG | CCCTCGCCCT  | TGCTGCTGAT | CCCGCTTG   | GAGGAA     | AGCATT   | AGAAATG | 120 |
| Db | 316 | TCATCGATGAG | CCCTCGCCCT  | TGCTGCTGAT | CCCGCTTG   | GAGGAA     | AGCATT   | AGAAATG | 375 |
| QY | 121 | AATTGATCTGT | TCTTAAAGGAT | GGGACAGAAA | CAGATCCT   | GTGTGAT    | TATTTAT  | TGTG    | 180 |
| Db | 376 | AATTGATCTGT | TCTTAAAGGAT | GGGACAGAAA | CAGATCCT   | GTGTGAT    | TATTTAT  | TGTG    | 435 |
| QY | 181 | AACGGGATTAC | AGATTGAAAT  | GGAAGTCAC  | CAAAAGTGC  | ATTACAT    | TGACAG   | AGAAAAC | 240 |
| Db | 436 | AACGGGATTAC | AGATTGAAAT  | GGAAGTCAC  | CAAAAGTGC  | ATTACAT    | TGACAG   | AGAAAAC | 494 |

|                           |   |  |                            |
|---------------------------|---|--|----------------------------|
| Oy                        | 241   | AGACGAGAAATCTTGATGGCTTCAACAAGACATGAAC                          | 278                        |
|                           |   |  |                            |
| Db                        | 495   | AGACGAGAAATCTTGATGGCTTCAACAAGATGCAC                            | 532                        |
| <hr/>                     |   |  |                            |
| RESULT 10                 |   |  |                            |
| LOCUS                     | BD082483  | 1872 bp  | DNA linear PAT 27-AUG-2002 |
| DEFINITION                | PCs3, PCs genes, and methods of use.                |  |                            |
| ACCESSION                 | BD082483.1  | GI:22628093  |                            |
| VERSION                   | JP 2001522240-A/2.                                  |  |                            |
| KEYWORDS                  | Mastadenovirus                                      |  |                            |
| SOURCE                    | Mastadenovirus                                      |  |                            |
| ORGANISM                  | Viruses; dsDNA viruses, no RNA stage; Adenoviridae. |  |                            |
| REFERENCE                 | 1 (bases 1 to 1872)                                 |  |                            |
| AUTHORS                   | Bussemakers,M,J.G.                                  |  |                            |
| TITLE                     | PCs3, PCs genes, and methods of use                 |  |                            |
| JOURNAL                   | Patent: JP 2001522240-A 2 13-NOV-2001;              |  |                            |
| COMMENT                   | DIAGNOCURE INC                                      |  |                            |
|                           | PJ  | JP 2001522240-A/2  |                            |
|                           | PD  | 13-NOV-2001  |                            |
|                           | PF  | 09-APR-1998 JP 1998542194                                      |                            |
|                           | PR  | 10-APR-1997 US 60/041836                                       |                            |
|                           | PI  | MARTON J G, BUSSEMAKERS  |                            |
|                           | PC  | C12N15/00,C12N15/12,C12N5/12,C12N1/21,C07K14/47,C07K16/18, PC  |                            |
|                           |   | C12Q1/68,  |                            |
|                           | PC  | G01N33/577,A61K39/395,A01K67/027                               |                            |
|                           | CC  | Strandedness: Double;  |                            |
|                           | CC  | Topology: Linear;  |                            |
|                           | FH  | Key Location/Qualifiers.                                       |                            |
| FEATURES                  |   |  |                            |
| source                    | 1..1872   |  |                            |
|                           | /organism="Mastadenovirus"                          |  |                            |
|                           | /mol_type="Genomic DNA"                             |  |                            |
|                           | /db_xref="taxon:10509"                              |  |                            |
| BASE COUNT                | 567 a   | 389 c  | 369 g 539 t 8 others       |
| ORIGIN                    |   |  |                            |
| Query Match               | 95.7%; Score 266; DB 6; Length 1872;                |  |                            |
| Best Local Similarity     | 99.6%; Pred.No.2,2e-68;                             |  |                            |
| Matches 277; Conservative | 0;  | Mismatches 0;  | Indels 1; Gaps 1;          |
| Oy                        | 1   | CAGAGAACAACAAAAGAAAGCACAAGATCCCTGGAGAAATGCCCGCCCATCTTTGGG      | 60                         |
| Db                        | 256   | CAGAGAACAACAAAAGAAAGCACAAGATCCCTGGAGAAATGCCCGCCCATCTTTGGG      | 315                        |
| Oy                        | 61  | TCATGTGATGAGCCTTCGCCCTGTGCTGTGCTTCGCCCTTGTGAGGAAAGACATTAGAAATG | 120                        |
| Db                        | 316   | TCATGTGATGAGCCTTCGCCCTGTGCTGTGCTTCGCCCTTGTGAGGAAAGACATTAGAAATG | 375                        |
| Oy                        | 121   | AATTGATGTGTTCCCTTAAGATGGGACGAAAAACAGATCCGTGTGATGATTTAATTG      | 180                        |
| Db                        | 376   | AATTGATGTGTTCCCTTAAGATGGGACGAAAAACAGATCCGTGTGATGATTTAATTG      | 435                        |
| Oy                        | 181   | AACGGATTACAGATTGGAATGAAGTCAACCMAAGTGAATTAACAATGAGAGAAAAC       | 240                        |
| Db                        | 436   | AACGGATTACAGATTGGAATGAAGTCA-CAAAGTGAATTAACAATGAGAGAAAAC        | 494                        |
| Oy                        | 241   | AGACGAGAAATCTTGATGGCTTCAACAAGACATGCAAC                         | 278                        |
| Db                        | 495   | AGACGAGAAATCTTGATGGCTTCAACAAGACATGCAAC                         | 532                        |
| <hr/>                     |   |  |                            |
| RESULT 11                 |   |  |                            |
| LOCUS                     | BD082482  | 2037 bp  | DNA linear PAT 27-AUG-2002 |
| DEFINITION                | PCAs3, PCs3 genes, and methods of use.              |  |                            |
| ACCESSION                 | BD082482.1  | GI:22628092  |                            |
| VERSION                   | JP 2001522240-A/1.                                  |  |                            |
| KEYWORDS                  | Mastadenovirus                                      |  |                            |
| SOURCE                    | Mastadenovirus                                      |  |                            |
| ORGANISM                  | Mastadenovirus                                      |  |                            |

| REFERENCE   | TITLE   | AUTHORS   | JOURNAL   | COMMENT   |
|---|---|---|-----------|---|
| 1 (bases 1 to 2037)   |   | Bussemakers, M.U.G.                                       |           | Viruses: dsDNA viruses, no RNA stage; Adenoviridae. |
| PCa3, PCa3 genes, and methods of use  |   |   |           |   |
| Patent: JP 2001522240-A 1 13-NOV-2001;  |   |   |           |   |
| DIAGNOSTIC INC SECRETARY OF THE DEPARTMENT OF HEALTH HUMAN SERVICES             |   |   |           |   |
| PN JP 2001522240-A/1  |   |   |           |   |
| PD 13-NOV-2001  |   |   |           |   |
| PF 09-APR-1998 JP 1998542194  |   |   |           |   |
| PR 10-APR-1997 US 60/041836   |   |   |           |   |
| PI MARION J G BUSSEMAKERS   |   |   |           |   |
| PC C12N15/00, C12N15/12, C12N5/12, C12N1/21, C07K14/47, C07K16/18, PC C1201/68. |   |   |           |   |
| CC G01N33/577, A61K39/395, A01K67/027   |   |   |           |   |
| CC Strandedness: Double;  |   |   |           |   |
| CC Topology: Linear;  |   |   |           |   |
| CC Key  |   |   |           |   |
| FT CDS  |   |   |           |   |
| Location/Qualifiers   |   |   |           |   |
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| /organism="Mastadenovirus"  |   |   |           |   |
| /mol_type="genomic DNA"   |   |   |           |   |
| /db_xref="taxon:10509"  |   |   |           |   |
| BASE COUNT  | 622 a   | 426 c   | 406 g     | 575 t   |
| ORIGIN  |   |   |           | 8 others  |
| Query Match   | 95.7%   | Score 266;  | DB 6;     | Length 2037;  |
| Best Local Similarity   | 99.6%;  | Pred. No. 2.2e-68;  |           |   |
| Matches 277;  | Conservative 0;   | Mismatches 0;   | Indels 1; | Gaps 1;   |
| QY  | 1   | CAGGAGCACAAGAAAGAAAGCAGAGATCCCTGGAGAAATGCCGCGCCGATCTTGGG  | 60        |   |
| DB  | 421   | CAGGAGCACAAGAAAGAAAGCAGAGATCCCTGGAGAAATGCCGCGCCGATCTTGGG  | 480       |   |
| QY  | 61  | TCATCGATGAGCCTCGCCCTGCGCTGGTCCCGCTTGAGGAAAGACATTAGAAATG   | 120       |   |
| DB  | 481   | TCATCGATGAGCCTCGCCCTGCGCTGGTCCCGCTTGAGGAAAGACATTAGAAATG   | 540       |   |
| QY  | 121   | AATTGATGTGTTCTTAAAGATGGGACAGAAAACAGATCCTGTGTGGATATTTATTTG | 180       |   |
| DB  | 541   | AATTGATGTGTTCTTAAAGATGGGACAGAAAACAGATCCTGTGTGGATATTTATTTG | 600       |   |
| QY  | 181   | AACGGGATTAACAGATTGAAATGAATGACCAAAAGTAGCATTTACCATGAGAGAAAC | 240       |   |
| DB  | 601   | AACGGGATTAACAGATTGAAATGAATGACCAAAAGTAGCATTTACCATGAGAGAAAC | 659       |   |
| QY  | 241   | AGACGAGAAATCTTGATGGCTTACCAAGACATGCAAC                     | 278       |   |
| DB  | 660   | AGACGAGAAATCTTGATGGCTTACCAAGACATGCAAC                     | 657       |   |
| RESULT 12   |   |   |           |   |
| AR261037/c  |   |   |           |   |
| LOCUS   | AR261037  | 2229 bp   | DNA       | linear  |
| DEFINITION  | Sequence 469 from patent US 6321716.                              |   |           |   |
| ACCESSION   | AR261037  |   |           |   |
| VERSION   | AR261037.1  | GI:28071800   |           |   |
| KEYWORDS  |   |   |           |   |
| SOURCE  | Unknown.  |   |           |   |
| ORGANISM  | Unclassified.   |   |           |   |
| REFERENCE   | 1 (bases 1 to 2229)   |   |           |   |
| AUTHORS   | Mashiki, Z. and Harada, J.  |   |           |   |
| TITLE   | Negative pressure control apparatus for engine mounted in vehicle |   |           |   |
| JOURNAL   | Patent: US 6321716-A-469 27-NOV-2001;                             |   |           |   |
| FEATURES  | Location/Qualifiers   |   |           |   |
| source  | 1..2229   |   |           |   |
| BASE COUNT  | 654 a   | 447 c   | 481 g     | 647 t   |
| ORIGIN  |   |   |           |   |
| Query Match   | 95.7%   | Score 266;  | DB 6;     | Length 2229;  |
| Best Local Similarity   | 99.6%;  | Pred. No. 2.2e-68;  |           |   |



Query Match 95.7%; Score 266; DB 6; Length 2229;  
Best Local Similarity 99.6%; Pred. No. 2.2e-68;  
Matches 277; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

|    |      |   |      |
|----|------|---|------|
| QY | 1    | CAGGAAGCACAAGAGAGACAGATCCCTGGAGAAATGCCGCGCCCATCTTGGG    | 60   |
| DB | 1617 | CAGGAAGCACAAGAGAGACAGATCCCTGGAGAAATGCCGCGCCCATCTTGGG    | 1558 |
| QY | 61   | TCATCGATGAGCCTCGCCCTGTGCTGCTCCGCTTGTGAGGAGACATTAGAAAATG | 120  |
| DB | 1557 | TCATCGATGAGCCTCGCCCTGTGCTGCTCCGCTTGTGAGGAGACATTAGAAAATG | 1498 |
| QY | 121  | AATTGATGTGTCCTTAAGAGATGGCAGAAAAACAGATCCTGTGTGATATTATTG  | 180  |
| DB | 1497 | AATTGATGTGTCCTTAAGAGATGGCAGAAAAACAGATCCTGTGTGATATTATTG  | 1438 |
| QY | 181  | AACGGATTACAGATTGAAATGAAGTCAACCAAGTACGATTACCAATGAGAGAAAC | 240  |
| DB | 1437 | AACGGATTACAGATTGAAATGAAGTCA-CAAAGTACGATTACCAATGAGAGAAAC | 1379 |
| QY | 241  | AGACGAGAAATCTTGATGGCTTCACAAAGACATGCAAC                  | 278  |
| DB | 1378 | AGACGAGAAATCTTGATGGCTTCACAAAGACATGCAAC                  | 1341 |

Search completed: February 1, 2004, 10:18:49  
Job time : 1515 secs



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OM nucleic - nucleic search, using sw model

Run on: February 1, 2004, 09:37:31 / Search time 49 Seconds  
(without alignments)  
2504.174 Million cell updates/sec

Title: US-09-675-650-2

Perfect score: 278

Sequence: 1 caggagcacaagaagc.....ggctccacaagacatgcac 278

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*  
1: /cgn2\_6/ptocdata/1/ina/5A COMB.seq:\*  
2: /cgn2\_6/ptocdata/1/ina/5B COMB.seq:\*  
3: /cgn2\_6/ptocdata/1/ina/6A COMB.seq:\*  
4: /cgn2\_6/ptocdata/1/ina/6B COMB.seq:\*  
5: /cgn2\_6/ptocdata/1/ina/PCFUS COMB.seq:\*  
6: /cgn2\_6/ptocdata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 266   | 95.7        | 812    | 4  | US-09-439-313-471  |
| 2          | 266   | 95.7        | 812    | 4  | US-09-352-616A-471 |
| 3          | 266   | 95.7        | 2229   | 4  | US-09-439-313-469  |
| 4          | 266   | 95.7        | 2229   | 4  | US-09-352-616A-469 |
| 5          | 266   | 95.7        | 2426   | 4  | US-09-439-313-470  |
| 6          | 266   | 95.7        | 2426   | 4  | US-09-352-616A-470 |
| 7          | 266   | 95.7        | 3112   | 4  | US-09-439-313-468  |
| 8          | 266   | 95.7        | 3112   | 4  | US-09-352-616A-468 |
| 9          | 241   | 86.7        | 718    | 4  | US-09-439-313-313  |
| 10         | 241   | 86.7        | 718    | 4  | US-09-352-616A-313 |
| 11         | 241   | 86.7        | 718    | 4  | US-09-232-149A-313 |
| 12         | 61    | 21.9        | 301    | 4  | US-09-439-313-287  |
| 13         | 61    | 21.9        | 301    | 4  | US-09-352-616A-287 |
| 14         | 61    | 21.9        | 301    | 4  | US-09-232-149A-287 |
| 15         | 36    | 12.9        | 7218   | 1  | US-08-232-463-14   |
| 16         | 35    | 12.6        | 10207  | 1  | US-08-920-812-2    |
| 17         | 35    | 12.6        | 10207  | 1  | US-08-920-827-2    |
| 18         | 35    | 12.6        | 10207  | 1  | US-08-921-177-2    |
| 19         | 35    | 12.6        | 10207  | 1  | US-08-362-577C-2   |
| 20         | 35    | 12.6        | 10207  | 2  | US-08-920-828-2    |
| 21         | 33.8  | 12.2        | 1113   | 4  | US-09-134-001C-139 |
| 22         | 32.2  | 11.6        | 2427   | 4  | US-09-601-198-70   |
| 23         | 31.4  | 11.3        | 1020   | 4  | US-09-007-288E-118 |
| 24         | 30.6  | 11.0        | 4758   | 3  | US-09-191-647-1    |
| 25         | 30.6  | 11.0        | 4758   | 3  | US-09-540-245A-1   |
| 26         | 30.6  | 11.0        | 4758   | 3  | US-09-540-153-1    |
| 27         | 30.4  | 10.9        | 5428   | 4  | US-09-625-972-21   |

|    |      |      |         |   |                     |                   |
|----|------|------|---------|---|---------------------|-------------------|
| 28 | 30.4 | 10.9 | 9641    | 4 | US-09-625-972-22    | Sequence 22, Appl |
| 29 | 29.4 | 10.6 | 2085    | 2 | US-08-668-128B-7    | Sequence 7, Appl  |
| 30 | 29.4 | 10.6 | 2085    | 2 | US-08-905-445-7     | Sequence 7, Appl  |
| 31 | 29.4 | 10.6 | 5857    | 4 | US-09-220-133-79    | Sequence 79, Appl |
| 32 | 29.2 | 10.5 | 152331  | 3 | US-09-128-155-16    | Sequence 16, Appl |
| 33 | 29.2 | 10.5 | 176373  | 3 | US-09-128-155-17    | Sequence 17, Appl |
| 34 | 29.2 | 10.5 | 580073  | 4 | US-08-545-528D-1    | Sequence 1, Appl  |
| 35 | 29.2 | 10.5 | 1830121 | 4 | US-09-557-884-1     | Sequence 1, Appl  |
| 36 | 29.2 | 10.5 | 1830121 | 4 | US-09-643-990A-1    | Sequence 1, Appl  |
| 37 | 28.8 | 10.4 | 360     | 4 | US-09-107-532A-1113 | Sequence 1113, Ap |
| 38 | 28.8 | 10.4 | 1022    | 3 | US-08-960-780-33    | Sequence 33, Appl |
| 39 | 28.8 | 10.4 | 1022    | 3 | US-09-073-898-33    | Sequence 33, Appl |
| 40 | 28.8 | 10.4 | 1952    | 1 | US-08-333-358-1     | Sequence 1, Appl  |
| 41 | 28.8 | 10.4 | 1952    | 1 | US-08-463-694-1     | Sequence 1, Appl  |
| 42 | 28.8 | 10.4 | 1952    | 1 | US-08-694-501-1     | Sequence 1, Appl  |
| 43 | 28.8 | 10.4 | 3460    | 2 | US-08-751-305-1     | Sequence 1, Appl  |
| 44 | 28.8 | 10.4 | 4074    | 1 | US-08-471-033-19    | Sequence 19, Appl |
| 45 | 28.8 | 10.4 | 4074    | 2 | US-08-471-044-19    | Sequence 19, Appl |

## ALIGNMENTS

|  |                                     |
|--|-------------------------------------|
| RESULT 1   | US-09-439-313-471/c                 |
| Sequence 471, Application US/09439313                        |                                     |
| Patent No. 6329505   |                                     |
| GENERAL INFORMATION:   |                                     |
| APPLICANT: Xu, Jiangchun                                     |                                     |
| APPLICANT: Dillon, Davin C.                                  |                                     |
| APPLICANT: Mitcham, Jennifer L.                              |                                     |
| APPLICANT: Harlocker, Susan Louise                           |                                     |
| APPLICANT: Jiang Yugui.                                      |                                     |
| APPLICANT: Reed, Steven G.                                   |                                     |
| APPLICANT: Kaelos, Michael                                   |                                     |
| APPLICANT: Rafter, Gary                                      |                                     |
| APPLICANT: Retter, Mark                                      |                                     |
| APPLICANT: Solik, John                                       |                                     |
| APPLICANT: Day, Craig  |                                     |
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND |                                     |
| FILE REFERENCE: 210121.42709                                 |                                     |
| CURRENT APPLICATION NUMBER: US/09/439,313                    |                                     |
| CURRENT FILING DATE: 1999-11-12                              |                                     |
| NUMBER OF SEQ ID NOS: 575                                    |                                     |
| SOFTWARE: FASTSEQ for Windows Version 3.0                    |                                     |
| SEQ ID NO 471  |                                     |
| LENGTH: 812  |                                     |
| TYPE: DNA  |                                     |
| ORGANISM: Homo sapiens                                       |                                     |
| Query Match  | 95.7%; Score 266; DB 4; Length 812; |
| Best Local Similarity  | 99.6%; Pred. No. 9.2e-80;           |
| Matches 277; Conservative                                    | 0; Mismatches 0; Indels 1; Gaps 1;  |
| US-09-439-313-471  |                                     |
| 1 CAGGAGCCAAAGAGACAGAGATCCCTGGGGAATGCCGCCGCACTTTGGG          | 60                                  |
| 562 CAGGAGCCAAAGAGACAGAGATCCCTGGGGAATGCCGCCGCACTTTGGG        | 503                                 |
| 61 TCATCATGATGCTCTTAAGATGGGACAGAAACAGATCTGTTGATTTAATTG       | 120                                 |
| 502 TCATCATGATGCTCTTAAGATGGGACAGAAACAGATCTGTTGATTTAATTG      | 443                                 |
| 121 AATTGATGCTCTTAAGATGGGACAGAAACAGATCTGTTGATTTAATTG         | 180                                 |
| 442 AATTGATGCTCTTAAGATGGGACAGAAACAGATCTGTTGATTTAATTG         | 383                                 |
| 181 AAGGATTAACGATTTGAATGAATCAACAAAGAGACATTAACAAAGAGAAAC      | 240                                 |
| 382 AAGGATTAACGATTTGAATGAATCAACAAAGAGACATTAACAAAGAGAAAC      | 324                                 |
| 241 AGAGAGAAATCTGATGGCTTCAACAAGATGAAC 278                    |                                     |





| QY | 61   | CGATGATGACCTCGCCCTGTGCCTGGTTCGCGCTGTGAGAGAAAGACATTAGAAAATG  | 120  |
|----|------|---|------|
| Db | 1531 | TCATCGATGACCTCGCCCTGTGCCTGGTTCGCGCTGTGAGAGAGACATTAGAAAATG   | 1590 |
| QY | 121  | AATTGATGTGTTCCCTTAAAGATGGGACAGAAAACAGATCCGTGTGTGATATTATTG   | 180  |
| Db | 1591 | AATTGATGTGTTCCCTTAAAGATGGGACAGAAAACAGATCCGTGTGTGATATTATTG   | 1650 |
| QY | 181  | AACGGGATTACAGATTTGAAATGAAGTCACCAAATGACATTACCAATGAGAGAAAAC   | 240  |
| Db | 1651 | AACGGGATTACAGATTTGAAATGAAGTCA-CAAATGAGCAATTACCAATGAGAGAAAAC | 1709 |
| QY | 241  | AGACGAGAAATCTTGATGGCTCCCAAGACACATGCAAC                      | 278  |
| Db | 1710 | AGACGAGAAATCTTGATGGCTCCCAAGACACATGCAAC                      | 1747 |

```

RESULT 8
US-09-352-616A-468
Sequence 468, Application US/09352616A
Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yugu
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.42768
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 468
LENGTH: 3112
TYPE: DNA
ORGANISM: Homo sapiens
US-09-352-616A-468

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|                       |              |                    |               |                   |
|-----------------------|--------------|--------------------|---------------|-------------------|
| Query Match           | 95.7%        | Score 266;         | DB 4;         | Length 3112;      |
| Best Local Similarity | 99.6%        | Pred. No. 1.8e-79; |               |                   |
| Matches 277;          | Conservative | 0;                 | Mismatches 0; | Indels 1; Gaps 1; |

|    |      |                        |                                     |      |
|----|------|------------------------|-------------------------------------|------|
| Qy | 1    | CAGAGAAGCAAAAAGGAAGCA  | CAGAGATCTCCGGAGAAATGCCCGCGCCATCTTG  | 60   |
| Db | 1471 | CAGAGAAGCAAAAAGGAAGCA  | CAGAGATCTCCGGAGAAATGCCCGCGCCATCTTG  | 1530 |
| Qy | 61   | TCATCGATGAGCTTCGCCCTG  | CTGCTGCCCTTGTGAGGAGNCAATTAGAAATG    | 120  |
| Db | 1531 | TCATCGATGAGCTTCGCCCTG  | CTGCTGCCCTTGTGAGGAGNCAATTAGAAATG    | 1590 |
| Qy | 121  | AATTGATGTGTTCTTAAAGATG | GCGAGAAAAAGATCCCTGTGTGATTAATTATG    | 180  |
| Db | 1591 | AATTGATGTGTTCTTAAAGATG | GCGAGAAAAAGATCCCTGTGTGATTAATTATG    | 1650 |
| Qy | 181  | AACGGGATTCAGATTGAAATGA | AGTCAACCAAGTGACATTACCAATGAGAGAAAAAC | 240  |
| Db | 1651 | AACGGGATTCAGATTGAAATGA | AGTCAACCAAGTGACATTACCAATGAGAGAAAAAC | 1700 |
| Qy | 241  | AGACGAGAAATCTTGATGCGCT | CAAGACATGTGAAC                      | 278  |
| Db | 1710 | AGACGAGAAATCTTGATGCGCT | CAAGACATGTGAAC                      | 1747 |

RESULT 9  
US-09-439-313-313  
: Sequence 313, Application US/09439313  
: Patent No. 6329505  
: GENERAL INFORMATION:  
: APPLICANT: Xu, Jiangchun  
: APPLICANT: Dillon, Davin C.

```

: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan Louise
: APPLICANT: Jiang Yugu
: APPLICANT: Reed, Steven G.
: APPLICANT: Kalos, Michael
: APPLICANT: Fanger, Gary
: APPLICANT: Retter, Mark
: APPLICANT: Solk, John
: APPLICANT: Day, Craig
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
: FILE REFERENCE: 210121.427C9
: CURRENT APPLICATION NUMBER: US/09/439,313
: CURRENT FILING DATE: 1999-11-12
: NUMBER OF SEQ ID NOS: 575
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 313
: LENGTH: 718
: TYPE: DNA
: ORGANISM: Homo sapien
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (1)...(718)
: OTHER INFORMATION: n = A,T,C or G
US-09-439-313-313

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|                       |              |   |              |            |
|-----------------------|--------------|---|--------------|------------|
| Query Match           | 86.7%        | Score 241   | DB 4         | Length 718 |
| Best Local Similarity | 98.6%        | Pred. No. 2.2e-71   |              |            |
| Matches 274           | Conservative | 0   | Mismatches 1 | Indels 3   |
| Gaps                  |              |   |              | 3          |
| Qy                    | 1            | CAGGAGCACAAAAAGAAAGACAGAGATCCCTGGAGAGAAATGCCGCGCCGATCTTGGG      | 60           |            |
| Db                    | 231          | CAGGAGACACAAAAGAAAGACACAGATCCTTGGAGAAATGCCGCGCCGATCTTGGG        | 290          |            |
| Qy                    | 61           | TCATCGATGAGCCTCGCCCTGTGCTGCTGCCGCTTGTGAAGGAAAGACATTAGAAATG      | 120          |            |
| Db                    | 291          | TCATCGATGAGCCTCGCCCTGTGCTGCTGCCGCTTGTGAAGGAAAGACATTAGAAATG      | 350          |            |
| Qy                    | 121          | AATTGATGTGTTCTTCTTAAAGATGGGACAGAAAAACAGTCTCTGTGTGATATTATTTTG    | 180          |            |
| Db                    | 351          | AATTGATGTGTTCTTCTTAAAGAT-GGGACAGAAAAACAGTCTCTGTGTGATATTATTTTG   | 409          |            |
| Qy                    | 181          | AACGGATTACAGTTTGAATGAAATGAAATGCCAAAGTAGCATTTCCATTGAGAGGAAAAAC   | 240          |            |
| Db                    | 410          | AACGGATTACAGTTTGAATGAAATGAAATGCA-CAAAGTAGCATTTCCATTGAGAGGAAAAAC | 468          |            |
| Qy                    | 241          | AGACGAGAAATCTTGATGCGCTTACCAAGACATGCAAC                          | 278          |            |
| Db                    | 469          | AGACGAGAAATCTTGATGCG-TTACCAAGACATGCAAC                          | 505          |            |

```

RESULT 10
US-09-352-616A-313
Sequence 313, Application US/09352616A
Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yugu
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427/68
CURRENT APPLICATION NUMBER: US/09/352.616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 4/2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 313
LENGTH: 718
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:

```



Best Local Similarity 100.0%; Pred. No. 4.9e-11;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 218 AGCATTCACATGAGAGAAACAGACGAGAAATCTTGATGCTTCACAAAGCATGCA 277  
Db 301 AGCATTCACATGAGAGAAACAGACGAGAAATCTTGATGCTTCACAAAGCATGCA 242

QY 278 C 278  
Db 241 C 241

## RESULT 14

US-09-232-149A-287/C  
Sequence 287, Application US/09232149A  
Patent No. 6465611  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, David C.  
APPLICANT: Mitcham, Jennifer Lynn  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE  
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE  
FILE REFERENCE: 210121.427C6  
CURRENT APPLICATION NUMBER: US/09/232.149A  
NUMBER OF SEQ ID NOS: 338  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 287  
LENGTH: 301  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-232-149A-287

Query Match 21.9%; Score 61; DB 4; Length 301;  
Best Local Similarity 100.0%; Pred. No. 4.9e-11;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 218 AGCATTCACATGAGAGAAACAGACGAGAAATCTTGATGCTTCACAAAGCATGCA 277  
Db 301 AGCATTCACATGAGAGAAACAGACGAGAAATCTTGATGCTTCACAAAGCATGCA 242

QY 278 C 278  
Db 241 C 241

## RESULT 15

US-08-232-463-14/C  
Sequence 14, Application US/08232463  
Patent No. 5670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHEIFLINGER, F.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232.463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/935,313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BERT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-9300  
TELEFAX: (703) 683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: PTZ9Pt-F18  
US-08-232-463-14

## Query Match

Best Local Similarity 12.9%; Score 36; DB 1; Length 7218;  
Matches 6; Conservative 156; Mismatches 106; Indels 0; Gaps 0;

QY 2 AGAAGACACAAAAGAGACAGACAGATCCCTGGAGAAATGCCGCCCATCTTGCT 61

Db 1326 RRR 1267

QY 62 CATGATGAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 121

Db 1266 RRR 1207

QY 122 ATGATGCTGCTTAAAGATGCGAGCAAAACAGATCCTGCTGCTGCTGCTGCTGCT 181

Db 1206 RRR 1147

QY 182 ACGGATTACAGATTGAATGAGTACACAAAGTGAAGCATTCATGAGAGAAAGCA 241

Db 1146 RRR 1087

QY 242 GACGAGAAATCTTGATGCTTCACAG 269

Db 1086 RRR 1059

Search completed: February 1, 2004, 10:41:49  
Job time: 53 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using SW model

Run on: February 1, 2004, 09:50:21 ; Search time 222 Seconds  
(without alignments)  
4563.904 Million cell updates/sec

Title: US-09-675-650-2

Perfect score: 278

Sequence: 1 caggaagcacaagaagc.....ggttcacaagacatgcaac 278

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 2434939 seqs, 1822278265 residues

Total number of hits satisfying chosen parameters: 4869878

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: Published Applications\_NA:\*

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2: /cgn2\_6/ptodata/2/pubpna/PCR\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
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6: /cgn2\_6/ptodata/2/pubpna/PCRUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
14: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
17: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
18: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description                          |
|------------|-------|-------------|--------|----|--------------------------------------|
| C 1        | 266   | 95.7        | 812    | 9  | US-09-759-143-471 Sequence 471, App  |
| C 2        | 266   | 95.7        | 812    | 9  | US-09-780-669-471 Sequence 471, App  |
| C 3        | 266   | 95.7        | 812    | 9  | US-09-822-827-471 Sequence 471, App  |
| C 4        | 266   | 95.7        | 812    | 10 | US-09-895-793-471 Sequence 471, App  |
| C 5        | 266   | 95.7        | 812    | 10 | US-09-895-814-471 Sequence 471, App  |
| C 6        | 266   | 95.7        | 812    | 13 | US-10-144-678A-471 Sequence 471, App |
| C 7        | 266   | 95.7        | 812    | 13 | US-10-294-025-471 Sequence 471, App  |
| C 8        | 266   | 95.7        | 812    | 14 | US-10-294-025-471 Sequence 471, App  |
| C 9        | 266   | 95.7        | 812    | 15 | US-10-010-940-471 Sequence 471, App  |
| C 10       | 266   | 95.7        | 875    | 11 | US-09-957-708-3 Sequence 471, App    |
| C 11       | 266   | 95.7        | 2229   | 9  | US-09-759-143-469 Sequence 469, App  |
| C 12       | 266   | 95.7        | 2229   | 9  | US-09-780-669-469 Sequence 469, App  |
| C 13       | 266   | 95.7        | 2229   | 9  | US-09-822-827-469 Sequence 469, App  |
| C 14       | 266   | 95.7        | 2229   | 10 | US-09-895-793-469 Sequence 469, App  |
| C 15       | 266   | 95.7        | 2229   | 10 | US-09-895-814-469 Sequence 469, App  |

|      |     |      |      |    |                                      |
|------|-----|------|------|----|--------------------------------------|
| C 16 | 266 | 95.7 | 2229 | 13 | US-10-144-678A-469 Sequence 469, App |
| C 17 | 266 | 95.7 | 2229 | 13 | US-10-294-025-469 Sequence 469, App  |
| C 18 | 266 | 95.7 | 2229 | 14 | US-10-012-896-469 Sequence 469, App  |
| C 19 | 266 | 95.7 | 2229 | 15 | US-10-010-940-469 Sequence 469, App  |
| C 20 | 266 | 95.7 | 2229 | 15 | US-09-759-143-470 Sequence 470, App  |
| C 21 | 266 | 95.7 | 2426 | 9  | US-09-780-669-470 Sequence 470, App  |
| C 22 | 266 | 95.7 | 2426 | 9  | US-09-822-827-470 Sequence 470, App  |
| C 23 | 266 | 95.7 | 2426 | 10 | US-09-895-793-470 Sequence 470, App  |
| C 24 | 266 | 95.7 | 2426 | 10 | US-09-895-814-470 Sequence 470, App  |
| C 25 | 266 | 95.7 | 2426 | 13 | US-10-144-678A-470 Sequence 470, App |
| C 26 | 266 | 95.7 | 2426 | 13 | US-10-294-025-470 Sequence 470, App  |
| C 27 | 266 | 95.7 | 2426 | 14 | US-10-012-896-470 Sequence 470, App  |
| C 28 | 266 | 95.7 | 2426 | 15 | US-10-010-940-470 Sequence 470, App  |
| C 29 | 266 | 95.7 | 2426 | 15 | US-10-205-823-448 Sequence 468, App  |
| C 30 | 266 | 95.7 | 3112 | 9  | US-09-759-143-468 Sequence 468, App  |
| C 31 | 266 | 95.7 | 3112 | 9  | US-09-780-669-468 Sequence 468, App  |
| C 32 | 266 | 95.7 | 3112 | 9  | US-09-822-827-468 Sequence 468, App  |
| C 33 | 266 | 95.7 | 3112 | 10 | US-09-895-793-468 Sequence 468, App  |
| C 34 | 266 | 95.7 | 3112 | 10 | US-09-895-814-468 Sequence 468, App  |
| C 35 | 266 | 95.7 | 3112 | 13 | US-10-144-678A-468 Sequence 468, App |
| C 36 | 266 | 95.7 | 3112 | 13 | US-10-294-025-468 Sequence 468, App  |
| C 37 | 266 | 95.7 | 3112 | 14 | US-10-012-896-468 Sequence 468, App  |
| C 38 | 266 | 95.7 | 3112 | 15 | US-10-010-940-468 Sequence 468, App  |
| C 39 | 266 | 95.7 | 3223 | 9  | US-09-759-143-690 Sequence 690, App  |
| C 40 | 266 | 95.7 | 3223 | 9  | US-09-780-669-690 Sequence 690, App  |
| C 41 | 266 | 95.7 | 3223 | 9  | US-09-822-827-690 Sequence 690, App  |
| C 42 | 266 | 95.7 | 3223 | 10 | US-09-895-793-690 Sequence 690, App  |
| C 43 | 266 | 95.7 | 3223 | 10 | US-09-895-814-690 Sequence 690, App  |
| C 44 | 266 | 95.7 | 3223 | 13 | US-10-144-678A-690 Sequence 690, App |
| C 45 | 266 | 95.7 | 3223 | 13 | US-10-294-025-690 Sequence 690, App  |

#### ALIGNMENTS

RESULT 1  
US-09-759-143-471/C  
Sequence 471, Application US/09759143  
Patent No. US2002002248A1  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocke, Susan L.  
APPLICANT: Jjiang, Yuqun  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Ronger, Gary R.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Li, Samuel  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.427C23  
CURRENT APPLICATION NUMBER: US/09/759,143  
NUMBER OF SEQ ID NOS: 934  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 471  
LENGTH: 812  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-759-143-471  
Query Match 95.7%; Score 266; DB 9; Length 812;  
Best Local Similarity 99.6%; Pred. No. 9,7e-76;  
Matches 277; Conservative 0; Mismatches 0; Indels 1; Gaps 1;









QY 61 TCATCGATGAGCCTCGCCCTGCTGCTCCGCTTGTGAGGAGACATTAGAAAATG 120  
DB 1557 TCATCGATGAGCCTCGCCCTGCTGCTCCGCTTGTGAGGAGACATTAGAAAATG 1498  
QY 121 AATTGATGTGTTCTCTTAAAGGATGGGACGAAAAAGATCTGTGTGATATTATTG 180  
DB 1497 AATTGATGTGTTCTCTTAAAGGATGGGACGAAAAAGATCTGTGTGATATTATTG 1438  
QY 181 AACGGGATTACAGATTGAAATGAAGTCAACCAAGATGATTCACATGAGAGAAAAC 240  
DB 1437 AACGGGATTACAGATTGAAATGAAGTCA-CAAAGTGAAGATTCAATGAGAGAAAAC 1379  
QY 241 AGACGAGAAAATCTTGATGGCTTCACAAAGATGCAAC 278  
DB 1378 AGACGAGAAAATCTTGATGGCTTCACAAAGATGCAAC 1341

## RESULT 12

US-09-780-669-469/c  
Sequence 469, Application US/09780669  
Patent No. US20020051977A1

## GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yugu  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darick  
APPLICANT: Li, Samuel  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William  
APPLICANT: McNeill, John  
APPLICANT: Houghton, Raymond L.  
APPLICANT: Houghton, Raymond L.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
FILE REFERENCE: 210121.427C24  
CURRENT APPLICATION NUMBER: US/09/780.669  
CURRENT FILING DATE: 2001-02-09  
NUMBER OF SEQ ID NOS: 943  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 469  
LENGTH: 2229  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-780-669-469

Query Match 95.7%; Score 266; DB 9; Length 2229;  
Best Local Similarity 99.6%; Pred. No. 1.7e-75;

Matches 277; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CAGGAGCACAAGAGAGACAGAGATCCCTGGAGAAATGCCGCGCCGATCTTGGG 60  
DB 1617 CAGGAGCACAAGAGAGACAGAGATCCCTGGAGAAATGCCGCGCCGATCTTGGG 1558  
QY 61 TCATCGATGAGCCTCGCCCTGCTGCTCCGCTTGTGAGGAGACATTAGAAAATG 120  
DB 1557 TCATCGATGAGCCTCGCCCTGCTGCTCCGCTTGTGAGGAGACATTAGAAAATG 1498  
QY 121 AATTGATGTGTTCTCTTAAAGGATGGGACGAAAAAGATCTGTGTGATATTATTG 180  
DB 1497 AATTGATGTGTTCTCTTAAAGGATGGGACGAAAAAGATCTGTGTGATATTATTG 1438  
QY 181 AACGGGATTACAGATTGAAATGAAGTCAACCAAGATGATTCACATGAGAGAAAAC 240

DB 1437 AACGGGATTACAGATTGAAATGAAGTCA-CAAAGTGAAGATTCAATGAGAGAAAAC 1379  
QY 241 AGACGAGAAAATCTTGATGGCTTCACAAAGATGCAAC 278  
DB 1378 AGACGAGAAAATCTTGATGGCTTCACAAAGATGCAAC 1341

## RESULT 13

US-09-827-827-469/c  
Sequence 469, Application US/09822827  
Patent No. US20020081680A1

## GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yugu  
APPLICANT: Kalos, Michael D.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darick  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William T.  
APPLICANT: Henderson, Robert A.

Query Match 95.7%; Score 266; DB 9; Length 2229;  
Best Local Similarity 99.6%; Pred. No. 1.7e-75;

Matches 277; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CAGGAGCACAAGAGAGACAGAGATCCCTGGAGAAATGCCGCGCCGATCTTGGG 60  
DB 1617 CAGGAGCACAAGAGAGACAGAGATCCCTGGAGAAATGCCGCGCCGATCTTGGG 1558  
QY 61 TCATCGATGAGCCTCGCCCTGCTGCTCCGCTTGTGAGGAGACATTAGAAAATG 120  
DB 1557 TCATCGATGAGCCTCGCCCTGCTGCTCCGCTTGTGAGGAGACATTAGAAAATG 1498  
QY 121 AATTGATGTGTTCTCTTAAAGGATGGGACGAAAAAGATCTGTGTGATATTATTG 180  
DB 1497 AATTGATGTGTTCTCTTAAAGGATGGGACGAAAAAGATCTGTGTGATATTATTG 1438  
QY 181 AACGGGATTACAGATTGAAATGAAGTCAACCAAGATGATTCACATGAGAGAAAAC 240  
DB 1437 AACGGGATTACAGATTGAAATGAAGTCA-CAAAGTGAAGATTCAATGAGAGAAAAC 1379  
QY 241 AGACGAGAAAATCTTGATGGCTTCACAAAGATGCAAC 278  
DB 1378 AGACGAGAAAATCTTGATGGCTTCACAAAGATGCAAC 1341

## RESULT 14

US-09-895-793-469/c  
Sequence 469, Application US/09895793  
Patent No. US20020192763A1

## GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yugu  
APPLICANT: Kalos, Michael D.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darick  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William T.  
APPLICANT: Henderson, Robert A.

APPLICANT: Hural, John  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Houghton, Raymond L.  
APPLICANT: Vinals de Bassols, Carlota  
APPLICANT: Foy, Teresa  
APPLICANT: Fanger, Gary R.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.534C2  
CURRENT APPLICATION NUMBER: US/09/895,793  
CURRENT FILING DATE: 2001-06-29  
NUMBER OF SEQ ID NOS: 982  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 469  
LENGTH: 2229  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-895-793-469

Query Match 95.7%; Score 266; DB 10; Length 2229;  
Best Local Similarity 99.6%; Pred. No. 1.7e-75;  
Matches 277; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CAGGAAGCAGAAAGAGAGAGATCCCTGGAGAAATGCCCGCCCATCTTGGG 60  
DB 1617 CAGGAAGCAGAAAGAGAGAGATCCCTGGAGAAATGCCCGCCCATCTTGGG 1558  
QY 61 TCATCGATGAGCCTCGCCCTGTGCTGCTCCGCTTGTGAGGAGACATTGAAATG 120  
DB 1557 TCATCGATGAGCCTCGCCCTGTGCTGCTCCGCTTGTGAGGAGACATTGAAATG 1498  
QY 121 AATTGATGTGTTCTTAAAGATGGGAGAGAAACAGATCCTGTGTGATATTATTG 180  
DB 1497 AATTGATGTGTTCTTAAAGATGGGAGAGAAACAGATCCTGTGTGATATTATTG 1438  
QY 181 AACGGATTACAGATTGAAATGAGTCAACCAAGTAGGATTACCAATGAGAGAAAC 240  
DB 1437 AACGGATTACAGATTGAAATGAGTCA-CAAAGTAGGATTACCAATGAGAGAAAC 1379  
QY 241 AGACGAGAAATCTTGATGGCTTCACAAGACATGCAAC 278  
DB 1378 AGACGAGAAATCTTGATGGCTTCACAAGACATGCAAC 1341

RESULT 15  
US-09-895-814-469/c  
Sequence 469, Application US/09895814  
Publication No. US20020193296A1  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yugu  
APPLICANT: Kalos, Michael D.  
APPLICANT: Retter, Marc W.  
APPLICANT: Scolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darick  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William T.  
APPLICANT: Henderson, Robert A.  
APPLICANT: Hural, John  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Houghton, Raymond L.  
APPLICANT: Vinals de Bassols, Carlota  
APPLICANT: Foy, Teresa  
APPLICANT: Fanger, Gary R.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.427C26  
CURRENT APPLICATION NUMBER: US/09/895,814  
CURRENT FILING DATE: 2001-06-29  
NUMBER OF SEQ ID NOS: 990  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 469  
LENGTH: 2229  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-895-814-469

Query Match 95.7%; Score 266; DB 10; Length 2229;  
Best Local Similarity 99.6%; Pred. No. 1.7e-75;  
Matches 277; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CAGGAAGCAGAAAGAGAGAGATCCCTGGAGAAATGCCCGCCCATCTTGGG 60  
DB 1617 CAGGAAGCAGAAAGAGAGAGATCCCTGGAGAAATGCCCGCCCATCTTGGG 1558  
QY 61 TCATCGATGAGCCTCGCCCTGTGCTGCTCCGCTTGTGAGGAGACATTGAAATG 120  
DB 1557 TCATCGATGAGCCTCGCCCTGTGCTGCTCCGCTTGTGAGGAGACATTGAAATG 1498  
QY 121 AATTGATGTGTTCTTAAAGATGGGAGAGAAACAGATCCTGTGTGATATTATTG 180  
DB 1497 AATTGATGTGTTCTTAAAGATGGGAGAGAAACAGATCCTGTGTGATATTATTG 1438  
QY 181 AACGGATTACAGATTGAAATGAGTCAACCAAGTAGGATTACCAATGAGAGAAAC 240  
DB 1437 AACGGATTACAGATTGAAATGAGTCA-CAAAGTAGGATTACCAATGAGAGAAAC 1379  
QY 241 AGACGAGAAATCTTGATGGCTTCACAAGACATGCAAC 278  
DB 1378 AGACGAGAAATCTTGATGGCTTCACAAGACATGCAAC 1341

Search completed: February 1, 2004, 10:45:36  
Job time: 223 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2004, 09:35:11 ; Search time 1315 Seconds  
(without alignments)  
5138.133 Million cell updates/sec

Title: US-09-675-650-2

Perfect score: 278  
Sequence: 1 cagaagacacaaaggaagc.....ggcttcacaaagacatgcaac 278

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_estbun:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_png:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 165   | 59.4        | 167    | BF373406 | BF373406 IL2-FT015 |
| 2          | 119   | 42.8        | 402    | AA578773 | AA578773 nt24a0.8  |
| 3          | 43.6  | 15.7        | 489    | BG224987 | BG224987 kp52h05.Y |
| 4          | 41.4  | 14.9        | 1016   | BX442677 | BX442677 BX442677  |

| RESULT 1   | BF373406                  | 167 bp      | mrna                              | linear | EST 24-NOV-2000 |
|------------|---------------------------|-------------|-----------------------------------|--------|-----------------|
| LOCUS      | IL2-FT0159-070800-120-H01 | FT0159      | Homo sapiens cDNA, mRNA sequence. |        |                 |
| DEFINITION | BF373406                  |             |                                   |        |                 |
| ACCESSION  | BF373406.1                | GI:11335431 |                                   |        |                 |
| VERSION    |                           |             |                                   |        |                 |
| KEYWORDS   |                           |             |                                   |        |                 |
| SOURCE     |                           |             |                                   |        |                 |
| ORGANISM   |                           |             |                                   |        |                 |
| REFERENCE  |                           |             |                                   |        |                 |
| AUTHORS    |                           |             |                                   |        |                 |
| TITLE      |                           |             |                                   |        |                 |
| JOURNAL    |                           |             |                                   |        |                 |
| MEDLINE    |                           |             |                                   |        |                 |
| PubMed     |                           |             |                                   |        |                 |
| COMMENT    |                           |             |                                   |        |                 |

## ALIGNMENTS

BF373406 167 bp mrna linear EST 24-NOV-2000  
IL2-FT0159-070800-120-H01 FT0159 Homo sapiens cDNA, mRNA sequence.  
BF373406.1 GI:11335431  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 167)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.U.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,





| QY                    | 157  | GATCCTGTGGTGAGATTATTATTGTAACGGGATTCAGATTGGAATGACGACCAAGT   | 216                 |
|-----------------------|--|--|---------------------|
| Db                    | 542  | AAKARKKKKAKKAAKARKKAKMAAAAVKKKKMAAAMAAAAAMKKKAAAAAMAK      | 483                 |
| QY                    | 217  | GAGCATTAACCAATGAGAGAAAACGACGAGAAAATCTTGATGGCTTCACAGACA     | 272                 |
| Db                    | 482  | KAAAMKAAAMMMAMMMKAKKAAKMMAMMMAMKAAKMKKKMMMMKMMAMMMKMM      | 427                 |
| RESULT 6              | CNS02GLH   | 1029 bp  | DNA                 |
| LOCUS                 | CNS02GLH   |  |                     |
| DEFINITION            | Tetradon nigriviridis genome survey sequence T7 end of clone 13710 of library G from Tetradon nigriviridis, genomic survey sequence.   |  |                     |
| ACCESSION             | AL196478   | GI:7834628   |                     |
| VERSION               | AL196478.1   |  |                     |
| KEYWORDS              | GSS; genome survey sequence.   |  |                     |
| SOURCE                | Tetradon nigriviridis  |  |                     |
| ORGANISM              | Tetradon nigriviridis  |  |                     |
| REFERENCE             | 1 Roest Crolius,H., Jailton,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fitzmes,C., Winkler,P., Brothier,P., Quetier,F., Saurin,W. and Weissenbach,J. Estimate of human gene number provided by genome-wide analysis using Tetradon nigriviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)             |  |                     |
| AUTHORS               | 2 Roest Crolius,H., Jailton,O., Dasilva,C., Ozouf-Costaz,C., Fitzmes,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradon nigriviridis Genome Res. 10 (7), 935-945 (2000) |  |                     |
| JOURNAL               | 20359837   |  |                     |
| MEDLINE               | 10899143   |  |                     |
| PUBMED                | 3 (bases 1 to 1029)  |  |                     |
| REFERENCE             | Genoscope.   |  |                     |
| AUTHORS               | Direct Submission  |  |                     |
| TITLE                 | Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr   |  |                     |
| JOURNAL               | - Web : www.genoscope.cns.fr   |  |                     |
| COMMENT               | This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetradon nigriviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetradon.  |  |                     |
| FEATURES              | Location/Qualifiers  |  |                     |
| SOURCE                | 1..1029  |  |                     |
|                       | /organism="Tetradon nigriviridis"  |  |                     |
|                       | /mol_type="genomic DNA"  |  |                     |
|                       | /db_xref="taxon:99883"   |  |                     |
|                       | /clone="13710"   |  |                     |
|                       | /clone_lib="G"   |  |                     |
|                       | /note="Genoscope sequence ID : COAG137DF05LP1-end : T7"  |  |                     |
| BASE COUNT            | 300 a 66 c 233 g 211 t 219 others  |  |                     |
| ORIGIN                |  |  |                     |
| Query Match           | 14.4%  | Score 40;  | DB 29; Length 1029; |
| Best Local Similarity | 41.3%  | Pred. No. 2.6;   |                     |
| Matches               | 62;  | Mismatches 61;   | Indels 0; Gaps 0;   |
| QY                    | 103  | GAGGACATTGAAAATGAATGATGATGTCCTTAAGAGTGGGAGGAAAAACAGATCCT   | 162                 |
| Db                    | 839  | DAASAKAMTKAKCAKAKTKMTGTATTTATKACAAAAAMASGTGATTTAMAMATTTGTT | 898                 |
| QY                    | 163  | GTGTGGATATTATTATTGACGGGATTCACAGATTGGAATGAAGTCACCAAAAGTACAT | 222                 |

[illegible]

|            |   |  |             |
|------------|---|--|-------------|
| VERSION    | B1541137.1  |  | GI:15382249 |
| KEYWORDS   | EST   |  |             |
| SOURCE     | Bos taurus  |  |             |
| ORGANISM   | Bos taurus (cow)  |  |             |
| REFERENCE  | Smith, T.P.L., Groves, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Cnaas, E., Wray, V.E., White, J., Cho, V., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pette, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., and Keane, J.W.  |  |             |
| AUTHORS    | Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle  |  |             |
| TITLE      | Genome Res. 11 (4), 626-630 (2001)  |  |             |
| JOURNAL    | 21180013  |  |             |
| MEDLINE    | 11282978  |  |             |
| PUBMED     | Contact: Smith TPL  |  |             |
| COMMENT    | USDA, ARS, US Meat Animal Research Center<br>PO Box 166, Clay Center, NE 68933-0166, USA<br>Tel: 402 762 4366<br>Fax: 402 762 4390<br>Email: smitht@mail.marc.usda.gov<br>Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -mismore 18<br>-mismatch 12 options.<br>PCR primers<br>FORWARD: AGGAACAGCATGTAGCCAT<br>BACKWARD: GTTTCACGTACGACG<br>Plate: 119 row: I column: 22<br>Seq primer: ATTTAGGTGACACTATATG.<br>Location/Qualifiers<br>1..393<br>/organism="Bos taurus"<br>/mol_type="mRNA"<br>/db_xref="taxon:9913"<br>/tissue_type="pooled"<br>/lab_host="DH10B"<br>/clone_1lb="MARC 1BOV"<br>/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;<br>library made from pooled tissue from lymph node, ovary,<br>fat, hypothalamus, and pituitary."                       |  |             |
| FEATURES   | source  |  |             |
| BASE COUNT | 112 a 77 c 116 g 87 t 1 others  |  |             |
| ORIGIN     | Query Match 13.5% Score 37.4; DB 12; Length 393;<br>Best Local Similarity 58.0%; Pred. No. 11;<br>Matches 65; Conservative 0; Mismatches 47; Indels 0; Gaps 0;  |  |             |
| OY         | 82 TGCCGTGATCCCGCTGTGTGAGGGAAGGACATTAGAAATGATGTGTTCTTAAAGG 141<br>  |  |             |
| Db         | 217 TGCCCTTANAGAGTTTGAAGGTAATATCATTTGGGAAACAAATATATGAAACGAAGG 276<br>   |  |             |
| OY         | 142 ATGGGCGAGAAAACAGATCTCTGTTGTGATATTTATTGGAACGGATTACAG 193<br>   |  |             |
| Db         | 277 CTATATCTGGGAAACAGCTGTACTGTGGGAAACTTTTCAGAAATGATATACAG 328<br>   |  |             |
| RESULT 9   | AA815526 206 bp mRNA linear EST 13-FEB-1998   |  |             |
| LOCUS      | vp28c02.r1 Barstead mouse proximal colon MBLR86 Mus musculus cDNA   |  |             |
| DEFINITION | clone IMAGE:1077986 5', mRNA sequence.  |  |             |
| ACCESSION  | AA815526  |  |             |
| VERSION    | AA815526.1 GI:2885122   |  |             |
| KEYWORDS   | EST.  |  |             |
| SOURCE     | Mus musculus (house mouse)  |  |             |
| ORGANISM   | Mus musculus  |  |             |
| REFERENCE  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;<br>Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;<br>Bovidae; Bovinae; Bos.  |  |             |
| AUTHORS    | Smith, T.P.L., Groves, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Cnaas, E., Wray, V.E., White, J., Cho, V., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pette, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., and Keane, J.W.  |  |             |
| TITLE      | Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle  |  |             |
| JOURNAL    | Genome Res. 11 (4), 626-630 (2001)  |  |             |
| MEDLINE    | 21180013  |  |             |
| PUBMED     | 11282978  |  |             |
| COMMENT    | Contact: Smith TPL<br>USDA, ARS, US Meat Animal Research Center<br>PO Box 166, Clay Center, NE 68933-0166, USA<br>Tel: 402 762 4366<br>Fax: 402 762 4390<br>Email: smitht@mail.marc.usda.gov<br>Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -mismore 18<br>-mismatch 12 options.<br>PCR primers<br>FORWARD: AGGAACAGCATGTAGCCAT<br>BACKWARD: GTTTCACGTACGACG<br>Plate: 119 row: I column: 22<br>Seq primer: ATTTAGGTGACACTATATG.<br>Location/Qualifiers<br>1..393<br>/organism="Bos taurus"<br>/mol_type="mRNA"<br>/db_xref="taxon:9913"<br>/tissue_type="pooled"<br>/lab_host="DH10B"<br>/clone_1lb="MARC 1BOV"<br>/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;<br>library made from pooled tissue from lymph node, ovary,<br>fat, hypothalamus, and pituitary." |  |             |
| FEATURES   | source  |  |             |
| BASE COUNT | 112 a 77 c 116 g 87 t 1 others  |  |             |
| ORIGIN     | Query Match 13.5% Score 37.4; DB 12; Length 393;<br>Best Local Similarity 58.0%; Pred. No. 11;<br>Matches 65; Conservative 0; Mismatches 47; Indels 0; Gaps 0;  |  |             |
| OY         | 82 TGCCGTGATCCCGCTGTGTGAGGGAAGGACATTAGAAATGATGTGTTCTTAAAGG 141<br>  |  |             |
| Db         | 217 TGCCCTTANAGAGTTTGAAGGTAATATCATTTGGGAAACAAATATATGAAACGAAGG 276<br>   |  |             |
| OY         | 142 ATGGGCGAGAAAACAGATCTCTGTTGTGATATTTATTGGAACGGATTACAG 193<br>   |  |             |
| Db         | 277 CTATATCTGGGAAACAGCTGTACTGTGGGAAACTTTTCAGAAATGATATACAG 328<br>   |  |             |
| RESULT 9   | AA815526 206 bp mRNA linear EST 13-FEB-1998   |  |             |
| LOCUS      | vp28c02.r1 Barstead mouse proximal colon MBLR86 Mus musculus cDNA   |  |             |
| DEFINITION | clone IMAGE:1077986 5', mRNA sequence.  |  |             |
| ACCESSION  | AA815526  |  |             |
| VERSION    | AA815526.1 GI:2885122   |  |             |
| KEYWORDS   | EST.  |  |             |
| SOURCE     | Mus musculus (house mouse)  |  |             |
| ORGANISM   | Mus musculus  |  |             |
| REFERENCE  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;<br>Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;<br>Bovidae; Bovinae; Bos.  |  |             |
| AUTHORS    | Smith, T.P.L., Groves, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Cnaas, E., Wray, V.E., White, J., Cho, V., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pette, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., and Keane, J.W.  |  |             |
| TITLE      | Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle  |  |             |
| JOURNAL    | Genome Res. 11 (4), 626-630 (2001)  |  |             |
| MEDLINE    | 21180013  |  |             |
| PUBMED     | 11282978  |  |             |
| COMMENT    | Contact: Smith TPL<br>USDA, ARS, US Meat Animal Research Center<br>PO Box 166, Clay Center, NE 68933-0166, USA<br>Tel: 402 762 4366<br>Fax: 402 762 4390<br>Email: smitht@mail.marc.usda.gov<br>Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -mismore 18<br>-mismatch 12 options.<br>PCR primers<br>FORWARD: AGGAACAGCATGTAGCCAT<br>BACKWARD: GTTTCACGTACGACG<br>Plate: 119 row: I column: 22<br>Seq primer: ATTTAGGTGACACTATATG.<br>Location/Qualifiers<br>1..393<br>/organism="Bos taurus"<br>/mol_type="mRNA"<br>/db_xref="taxon:9913"<br>/tissue_type="pooled"<br>/lab_host="DH10B"<br>/clone_1lb="MARC 1BOV"<br>/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;<br>library made from pooled tissue from lymph node, ovary,<br>fat, hypothalamus, and pituitary." |  |             |
| FEATURES   | source  |  |             |
| BASE COUNT | 112 a 77 c 116 g 87 t 1 others  |  |             |
| ORIGIN     | Query Match 13.5% Score 37.4; DB 12; Length 393;<br>Best Local Similarity 58.0%; Pred. No. 11;<br>Matches 65; Conservative 0; Mismatches 47; Indels 0; Gaps 0;  |  |             |
| OY         | 82  |  |             |

| TITLE   | JOURNAL   | COMMENT  |
|---|---|--|
| Geisels, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Stepec, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R. |   |  |
| The WashU-HHMI Mouse EST Project  |   |  |
| Unpublished   |   |  |
| Contact: Marra M/Mouse EST Project  |   |  |
| WashU-HHMI Mouse EST Project  |   |  |
| Washington University School of Medicine  |   |  |
| 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108   |   |  |
| Tel: 314 286 1800   |   |  |
| Fax: 314 286 1810   |   |  |
| Email: mouseest@watson.wustl.edu  |   |  |
| This clone is available royalty-free through LNL; contact the   |   |  |
| IMAGE Consortium (info@image.lnl.gov) for further information.  |   |  |
| MG1:592282  |   |  |
| Sed primer: -28ml3 rev2 ET from Amersham.   |   |  |
| Location/Qualifiers   |   |  |
| 1. 206  |   |  |
| /organism="Mus musculus"  |   |  |
| /mol_type="mRNA"  |   |  |
| /strain="FVB/N"   |   |  |
| /db_xref="taxon:10090"  |   |  |
| /clone="IMAGE:1077986"  |   |  |
| /dev_stage="7 day juvenile"   |   |  |
| /lab_host="DH10B"   |   |  |
| /clone_id="Barstead mouse proximal colon MFLR6"   |   |  |
| /note="Vector: pT73D-Pac (Pharmacia) with a modified  |   |  |
| polylinker; Site 1: EcoRI; Site 2: NotI; 1st strand cDNA  |   |  |
| was primed with a Not I - oligo(dT) primer (5',   |   |  |
| TGTTACGATCTGAGGAGCGGCCCTTTTTTTTTTTTTTTTTTTTTTT  |   |  |
| 3'); double-stranded cDNA was ligated to Eco RI adaptors  |   |  |
| (AATTCGATCTTG), digested with Not I and cloned into the   |   |  |
| Not I and Eco RI sites of the modified pT73 vector.   |   |  |
| Library constructed by Bob Barstead."   |   |  |
| BASE COUNT  | 110 a   | 25 c 29 g 42 t   |
| ORIGIN  |   |  |
| Query Match   | 13.3%   | Score 37; DB 9; Length 206;                                  |
| Best Local Similarity   | 56.0%;  | Pred. No. 11;  |
| Matches   | 70;   | Conservative 0; Mismatches 55; Indels 0; Gaps 0;             |
| QY  | 127   | TGTTGTTCTTAAAGATGGGAGAGAAAAACAGATCTGTTGGATATTATTGAACGGG 186  |
| DB  | 66  | TGTTCTCACTCAAGATGGGAGAGGAAAGAACTCATGTGAAATCTAATAAATGAC 125   |
| QY  | 187   | ATTAACAGATTGAATGATGACCAAGAGAGCATTAACCAATGAGAGGAAACAGACGA 246 |
| DB  | 126   | CTTGGCCCTTTAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 185 |
| QY  | 247   | GAATA 251  |
| DB  | 186   | AAAAA 190  |
| RESULT 10   |   |  |
| AA170451  | 384 bp  | mRNA linear EST 24-DEC-1997                                  |
| LOCUS   | vt42f07.r1  | Barstead mouse proximal colon MFLR6 Mus musculus cDNA        |
| DEFINITION  | clone IMAGE:1165765 5', mRNA sequence.                                    |  |
| ACCESSION   | AA170451  |  |
| VERSION   | AA170451.1  | GI:2720369   |
| KEYWORDS  | EST.  |  |
| SOURCE  | Mus musculus (house mouse)  |  |
| ORGANISM  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;         |  |
| REFERENCE   | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.        |  |
| AUTHORS   | 1 (bases 1 to 384)  |  |
|   | Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., |  |
|   | Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,         |  |
|   | Schellenberg, K., Stepec, M., Tan, F., Underwood, K., Moore, B.,          |  |
|   | Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and           |  |
|   | Waterston, R.   |  |



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Tel: 352 392 4700  
Fax: 352 392 9704

Email: damej@mail.vetmed.ufl.edu  
Seq primer: M13 (-20) forward.

## FEATURES

source

1..811

/organism="Plasmodium berghei"

/mol\_type="mRNA"

/strain="ANKA clone 15cyl (clone of the ANKA 8417 HP clone

)"

/db\_xref="taxon:5821"

/dev\_stage="asynchronous blood stage"

/lab\_host="Swiss white mice"

/clone\_lib="Pb cDNA #20, Charles Yowell and Jane Carlton"

/note="Vector: Bluescript II vector DNA, excised from

Lambda ZAP II.; Site\_1: EcoRI, Site\_2: XhoI. Total RNA was

extracted from asynchronous blood stage forms of the

cloned ANKA isolate of P. berghei grown in laboratory

Swiss white mice. Contaminating host white cells had

previously been removed using a novel biomagnetic bead

protocol (J. Carlton et al., manuscript in preparation).

PolyA+ RNA was extracted and reverse transcribed using an

oligo dt-XhoI primer. Second strand cDNA was prepared

using RNase H and DNA polymerase I. EcoR I adaptors were

ligated to the cDNA, and it was digested with XhoI.

Fragments were size selected, and those between 1-5 kb

ligated into EcoRI/XhoI digested vector."

## BASE COUNT

260 a 144 c 171 g 224 t 12 others

## ORIGIN

Query Match 13.3%; Score 37; DB 10; Length 811;

Best Local Similarity 53.9%; Pred. No. 17;

Matches 76; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 9 ACAAAAGGAGCAGAGATCCTGGAGAATGCCGGCCGATCTTGGTCATCATG 68

Db 370 AGAAAAAGAAACAGAAAGCAGCTTCCAAATGAAAGCATCATTTGGGGCTTATAT 429

QY 69 GAGCCTCGCCCTGTGCTGCTGCTTGTGAGGAGAGCATTAGAAAATGAATTGATG 128

Db 430 TGTCTATTAATAATGATGATGTTGTCAGACATGTTGATTAAGACATTTCCAAAAAGGGGG 489

QY 129 TGTTCCTTAAGGATGGCGAG 149

Db 490 TGGCCCATACACCAAAAGAG 510

## RESULT 13

BZ819014 804 bp DNA linear GSS 18-MAR-2003

LOCUS PUGC0697B\_ZM\_0.6\_1.0\_KB Zea mays genomic clone ZMBRta337L17,

DEFINITION genomic survey sequence.

ACCESSION BZ819014

VERSION BZ819014.1 GI:29033836

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE 1 (bases 1 to 804)  
White, C.A., Quackenbush, J., Van Aken, S., Uterback, T., Resnick  
A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished

Other GSSs: PUGC0697D

Contact: Cathy Whitelaw

TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TR  
Class: sheared ends.

## FEATURES

source

1..804

/organism="Zea mays"

/mol\_type="genomic DNA"

/strain="B73"

/db\_xref="taxon:4577"

/clone\_lib="ZMBRta337L17"

/clone\_1b="ZM 0.6\_1.0 KB"

/note="Vector: pCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high

COT selected genomic DNA library"

## BASE COUNT

246 a 141 c 144 g 273 t

## ORIGIN

Query Match 13.2%; Score 36.8; DB 29; Length 804;

Best Local Similarity 51.2%; Pred. No. 19; Indels 0; Gaps 0;

Matches 86; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 99 GAGGAGAGACATTAGAAATGATGATGTTCTTAAGAGATGGCAGGAAACAGA 158

Db 310 GAGGATGAGAGCTACATATTAAGAAAAAGATGATTAAGAGATGAGGGGTAAAGGA 369

QY 159 TCTGTGTTGATATTATTGAAACGGATTTACAGATTGAATGAATGACCAAGTGA 218

Db 370 ATCTAGAGAAACAATCTAGTTTATTAGTTTCTTACACTTAACATTACAGAGCCMAATAG 429

QY 219 GCATTACCAATGAGAGAAACAGACAGAAATCTTGATGCTTCAC 266

Db 430 TGTGAACCAATTGAGATGACATGATTAACGATTTGCAATTAC 477

## RESULT 14

BZ819018 880 bp DNA linear GSS 18-MAR-2003

LOCUS PUGC0697D\_ZM\_0.6\_1.0\_KB Zea mays genomic clone ZMBRta337L17,

DEFINITION genomic survey sequence.

ACCESSION BZ819018

VERSION BZ819018.1 GI:29033840

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE 1 (bases 1 to 880)  
White, C.A., Quackenbush, J., Van Aken, S., Uterback, T., Resnick  
A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished

Other GSSs: PUGC0697B

Contact: Cathy Whitelaw

TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TR

Class: sheared ends.

Location/Qualifiers

1..880

/organism="Zea mays"

/mol\_type="genomic DNA"

/strain="B73"

/db\_xref="taxon:4577"

/clone\_1b="ZM 0.6\_1.0 KB"

/note="Vector: pCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high

COT selected genomic DNA library"

## BASE COUNT

297 a 157 c 158 g 268 t

## ORIGIN

Query Match

13.2%; Score 36.8; DB 29; Length 880;



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2004, 07:28:31 ; Search time 189 Seconds  
(without alignments)  
3970.602 Million cell updates/sec

Title: US-09-675-650-2

Perfect score: 278

Sequence: 1 caggaagcacaagaagc.....ggcttcaagaacatgcaac 278

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues 5105512

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: N\_Geneseq\_19Jun03:\*  
2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*  
3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*  
4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*  
5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*  
6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:\*  
7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:\*  
8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:\*  
9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\*  
10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:\*  
11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:\*  
12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:\*  
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20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*  
21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*  
22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*  
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*  
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:\*  
25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 278   | 100.0       | 278    | 22    | AAAF0667    |
| 2          | 266   | 95.7        | 812    | 21    | AAAF0667    |
| 3          | 266   | 95.7        | 812    | 22    | AAAF0667    |
| 4          | 266   | 95.7        | 812    | 22    | AAAF0667    |
| 5          | 266   | 95.7        | 812    | 22    | AAAF0667    |
| 6          | 266   | 95.7        | 812    | 22    | AAAF0667    |
| 7          | 266   | 95.7        | 812    | 22    | AAAF0667    |
| 8          | 266   | 95.7        | 812    | 24    | AAAF0667    |

|   |    |       |      |      |    |          |                    |
|---|----|-------|------|------|----|----------|--------------------|
| C | 9  | 266   | 95.7 | 812  | 25 | AAAF0667 | Prostate cancer th |
|   | 10 | 266   | 95.7 | 820  | 19 | AAAF0667 | Prostate cancer an |
|   | 11 | 266   | 95.7 | 876  | 24 | AAAF0667 | Human PSNA cDNA, P |
|   | 12 | 266   | 95.7 | 1872 | 21 | AAAF0667 | Prostate cancer an |
|   | 13 | 266   | 95.7 | 2037 | 19 | AAAF0667 | Prostate cancer an |
|   | 14 | 266   | 95.7 | 2229 | 21 | AAAF0667 | Human immunogenic  |
|   | 15 | 266   | 95.7 | 2229 | 22 | AAAF0667 | Human prostate cDN |
|   | 16 | 266   | 95.7 | 2229 | 22 | AAAF0667 | Human prostate-spe |
|   | 17 | 266   | 95.7 | 2229 | 22 | AAAF0667 | Human prostate-spe |
|   | 18 | 266   | 95.7 | 2229 | 22 | AAAF0667 | Prostate tumour an |
|   | 19 | 266   | 95.7 | 2229 | 22 | AAAF0667 | Human P710P invent |
|   | 20 | 266   | 95.7 | 2229 | 22 | AAAF0667 | Human P710P cDNA s |
|   | 21 | 266   | 95.7 | 2229 | 25 | AAAF0667 | Prostate cancer th |
|   | 22 | 266   | 95.7 | 2426 | 21 | AAAF0667 | Human immunogenic  |
|   | 23 | 266   | 95.7 | 2426 | 22 | AAAF0667 | Human prostate cDN |
|   | 24 | 266   | 95.7 | 2426 | 22 | AAAF0667 | Human prostate-spe |
|   | 25 | 266   | 95.7 | 2426 | 22 | AAAF0667 | Human prostate-spe |
|   | 26 | 266   | 95.7 | 2426 | 22 | AAAF0667 | Prostate tumour an |
|   | 27 | 266   | 95.7 | 2426 | 22 | AAAF0667 | Human P710P invent |
|   | 28 | 266   | 95.7 | 2426 | 24 | AAAF0667 | Human P710P cDNA s |
|   | 29 | 266   | 95.7 | 2426 | 25 | AAAF0667 | Prostate cancer th |
|   | 30 | 266   | 95.7 | 3112 | 21 | AAAF0667 | Human immunogenic  |
|   | 31 | 266   | 95.7 | 3112 | 22 | AAAF0667 | Human prostate cDN |
|   | 32 | 266   | 95.7 | 3112 | 22 | AAAF0667 | Human prostate-spe |
|   | 33 | 266   | 95.7 | 3112 | 22 | AAAF0667 | Human prostate-spe |
|   | 34 | 266   | 95.7 | 3112 | 22 | AAAF0667 | Prostate tumour an |
|   | 35 | 266   | 95.7 | 3112 | 22 | AAAF0667 | Human P710P invent |
|   | 36 | 266   | 95.7 | 3112 | 24 | AAAF0667 | Human P710P cDNA s |
|   | 37 | 266   | 95.7 | 3112 | 25 | AAAF0667 | Prostate cancer th |
|   | 38 | 266   | 95.7 | 3582 | 19 | AAAF0667 | Prostate cancer an |
|   | 39 | 266   | 95.7 | 3923 | 22 | AAAF0667 | Human CDNA encodin |
|   | 40 | 266   | 95.7 | 3923 | 22 | AAAF0667 | Gene D33 cDNA sequ |
|   | 41 | 266   | 95.7 | 3923 | 24 | AAAF0667 | Prostate cancer-as |
|   | 42 | 266   | 95.7 | 3923 | 24 | AAAF0667 | Human DD3 cDNA seq |
|   | 43 | 266   | 95.7 | 3923 | 25 | AAAF0667 | Prostate cancer th |
|   | 44 | 255.4 | 91.9 | 506  | 22 | AAAF0667 | Human differential |
|   | 45 | 241   | 86.7 | 718  | 21 | AAAF0667 | Human immunogenic  |

## ALIGNMENTS

|          |  |                         |
|----------|--|-------------------------|
| RESULT 1 | AAAF0667   | standard; cDNA, 278 BP. |
| ID       | AAAF0667   |                         |
| XX       | AAAF0667   |                         |
| AC       | AAAF0667   |                         |
| XX       | 11-JUN-2001  | (first entry)           |
| DT       | 11-JUN-2001  |                         |
| XX       | Human differentially expressed PCA3 cDNA (short form).             |                         |
| DE       | PCA3; prostate cancer; antigen; benign prostatic hyperplasia;      |                         |
| XX       | KW differential expression; diagnosis; gene therapy; chromosome 9; |                         |
| KW       | human; ss.   |                         |
| XX       |  |                         |
| OS       | Homo sapiens.  |                         |
| XX       |  |                         |
| XX       | Key  | Location/Qualifiers     |
| FT       | exon   | 1..26                   |
| FT       |  | /tag= a                 |
| FT       |  | /number= "3"            |
| FT       | exon   | 27..278                 |
| FT       |  | /tag= b                 |
| FT       |  | /number= "4a"           |
| XX       |  |                         |
| XX       | MO200123550-A2.  |                         |
| PN       | 05-APR-2001.   |                         |
| XX       |  |                         |
| PD       | 29-SEP-2000; 2000MO-CA01154.                                       |                         |
| XX       |  |                         |
| XX       | 29-SEP-1999; 99US-0156594.   |                         |

## (DIAG-) DIAGNOCURE, INC.

Basseo O, Cypre C, Fradet Y;

WPI; 2001-258132/26.

Novel nucleic acid encoding differentially expressed prostate cancer antigen 3 mRNA containing additional sequence giving rise to long PCA3 mRNA, useful for diagnosis of mammal afflicted with prostate cancer -

Example 1; Fig 3; 60pp; English.

The present sequence is that of an RT-PCR-amplified fragment of human prostate cancer antigen 3 (PCA3) mRNA. A 2nd amplified PCA3 sequence (see AAF30666) includes an additional 227 bp, inserted between exons 3 and 4a. The shorter form RNA is associated with prostate cancer whereas the longer form RNA is associated with a non-malignant prostatic state, such as benign prostatic hyperplasia. Based on the differential expression of these 2 PCA3 RNA species, protocols for the diagnosis of prostate disease are provided, including a method of diagnosing the presence or predisposition to develop prostate cancer in a patient. Also provided are therapeutic methods that use a nucleic acid encoding a differentially expressed PCA3 mRNA molecule, an antisense sequence, a protein encoded by a differentially expressed PCA3 mRNA, or an antibody raised against such a protein.

Sequence 278 BP; 90 A; 54 C; 75 G; 59 T; 0 other;

Query Match 100.0%; Score 278; DB 22; Length 278;

Best Local Similarity 100.0%; Pred. No. 3.7e-80;

Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CAGGAACACAAAGAAGACACAGATCCTGGAGAAATGCCCGCCCATCTTGGG 60
DB 1 CAGGAACACAAAGAAGACACAGATCCTGGAGAAATGCCCGCCCATCTTGGG 60
QY TCATCGATGAGCCTCGCCCTGTGCTGCTCCGCTTGAGAGGACATTAGAAATG 120
DB TCATCGATGAGCCTCGCCCTGTGCTGCTCCGCTTGAGAGGACATTAGAAATG 120
QY 121 AATTGATGTCTCTTAAGAGATGGGAGAAAACAGATCCTGTTGTGATATTATTG 180
DB 121 AATTGATGTCTCTTAAGAGATGGGAGAAAACAGATCCTGTTGTGATATTATTG 180
QY 181 AACGGATTACAGTTTGAATGAAGTCAACCAAGTGCATTACCAATGAGAGAAAC 240
DB 181 AACGGATTACAGTTTGAATGAAGTCAACCAAGTGCATTACCAATGAGAGAAAC 240
QY 241 AGACGAGAAAATCTTGATGGCTTCAACAAGATGCAC 278
DB 241 AGACGAGAAAATCTTGATGGCTTCAACAAGATGCAC 278
```

## RESULT 2

ID AAA06690 standard; cDNA; 812 BP.

AC AAA06690;

DT 13-JUN-2000 (first entry)

DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:471.

KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;

XX immunogenic; cystostatic; vaccine; ss.

OS Homo sapiens.

PN WO200004149-A2.

PD 27-JAN-2000.

```
XX 14-JUL-1999; 99WO-US15838.
PF
XX
```

```
PR 14-JUL-1998; 98US-0115453.
PR 14-JUL-1998; 98US-0116134.
PR 23-SEP-1998; 98US-0159812.
PR 23-SEP-1998; 98US-0159822.
PR 15-JAN-1999; 99US-0232149.
PR 15-JAN-1999; 99US-0232880.
PR 09-APR-1999; 99US-0288946.
```

```
XX
XX
XX (CORI-) CORIXA CORP.
```

```
XX
XX
XX Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;
XX
XX WPI; 2000-171268/15.
```

```
DR
XX
XX
XX New polypeptide useful for treating and diagnosing prostate cancer
XX comprises an immunogenic portion of prostate tumor protein -
```

```
PT
XX
XX Claim 1; Page 262; 263pp; English.
```

The present invention describes isolated polypeptides, comprising an immunogenic portion of a prostate tumour protein (PRP). The polypeptides and polynucleotides encoding them have cytostatic activity and can be used in vaccines and in gene therapy. The polypeptides and polynucleotides encoding them, antigen presenting cells which express the polypeptides, antibodies against the polypeptides and vaccines comprising them can be used for inhibiting the development of prostate cancer in a patient. The polypeptides can be used to generate antibodies or anti-idiotypic antibodies for passive immuno therapy. A portion of the polynucleotides encoding the polypeptides can be used as a probe or to modulate the expression of the polypeptides. AA06241 to AA06691 and CC AA08200 to AA08202 represent sequences used in the exemplification of the present invention.

Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;

Query Match 95.7%; Score 266; DB 21; Length 812;

Best Local Similarity 99.6%; Pred. No. 4.7e-76;

Matches 277; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY 1 CAGGAACACAAAGAAGACACAGATCCTGGAGAAATGCCCGCCCATCTTGGG 60
DB 562 CAGGAACACAAAGAAGACACAGATCCTGGAGAAATGCCCGCCCATCTTGGG 503
QY TCATCGATGAGCCTCGCCCTGTGCTGCTCCGCTTGAGAGGACATTAGAAATG 120
DB 61 TCATCGATGAGCCTCGCCCTGTGCTGCTCCGCTTGAGAGGACATTAGAAATG 120
QY 121 AATTGATGTCTCTTAAGAGATGGGAGAAAACAGATCCTGTTGTGATATTATTG 180
DB 442 AATTGATGTCTCTTAAGAGATGGGAGAAAACAGATCCTGTTGTGATATTATTG 180
QY 181 AACGGATTACAGTTTGAATGAAGTCAACCAAGTGCATTACCAATGAGAGAAAC 240
DB 382 AACGGATTACAGTTTGAATGAAGTCAACCAAGTGCATTACCAATGAGAGAAAC 324
QY 241 AGACGAGAAAATCTTGATGGCTTCAACAAGATGCAC 278
DB 323 AGACGAGAAAATCTTGATGGCTTCAACAAGATGCAC 286
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## RESULT 3

ID AAS63899 standard; cDNA; 812 BP.

AC AAS63899;

DT 29-JAN-2002 (first entry)

DE Human prostate cDNA sequence #433.

KW Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.  
 XX Homo sapiens.  
 OS  
 XX NO2001.73032-A2.  
 PN  
 XX 04-OCT-2001.  
 PD  
 XX 27-MAR-2001; 2001WO-US09919.  
 PF  
 XX 27-MAR-2000; 2000US-0536957.  
 PR 09-MAY-2000; 2000US-0568100.  
 PR 12-MAY-2000; 2000US-0570737.  
 PR 13-JUN-2000; 2000US-0593793.  
 PR 27-JUN-2000; 2000US-0605783.  
 PR 10-AUG-2000; 2000US-0636215.  
 PR 29-AUG-2000; 2000US-0651236.  
 PR 06-SEP-2000; 2000US-0657279.  
 PR 02-OCT-2000; 2000US-0679426.  
 PR 10-OCT-2000; 2000US-0685166.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;  
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;  
 PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;  
 XX  
 DR WPI; 2001-639232/73.  
 PT New human prostate-specific polypeptides and polynucleotides useful for  
 PT the diagnosis and treatment of cancer, especially prostate cancer -  
 XX  
 PS Claim 1; Page 386-387; 579pp; English.  
 XX  
 CC The invention relates to isolated prostate-specific  
 CC polynucleotides, polypeptides, fusion proteins of the polypeptides,  
 CC antibodies raised against the polypeptides (or antigenic epitopes  
 CC derived from them) and antigen-presenting cells expressing the  
 CC polypeptides. The antibodies are useful for detecting the presence of  
 CC cancer, especially prostate cancer. The polypeptides, polynucleotides and  
 CC the antigen-presenting cells are useful for stimulating and/or expanding  
 CC T cells specific for a tumour protein, and for inhibiting the development  
 CC of cancer especially prostate cancer. Compositions comprising the  
 CC polynucleotide and/or polypeptide are useful for stimulating an immune  
 CC response, and for treating cancer. The oligonucleotide is useful for  
 CC detecting cancer. The present sequence is a prostate specific  
 CC polynucleotide of the invention.  
 CC  
 XX Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;  
 SQ  
 Query Match 95.7%; Score 266; DB 22; Length 812;  
 Best Local Similarity 99.6%; Pred. No. 4.7e-76;  
 Matches 277; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 XX  
 QY 1 CAGGAACACAAAAGAGACACAGATCCCTGGAGAAATGCCCGCCGATCTTGGG 60  
 Db 562 CAGGAACACAAAAGAGACACAGATCCCTGGAGAAATGCCCGCCGATCTTGGG 503  
 QY 61 TCATCGATGAGCCTCGCCCTGTGCTGCTCCGCTTGTGAGGAGAGACATTAGAAAATG 120  
 Db 502 TCATCGATGAGCCTCGCCCTGTGCTGCTCCGCTTGTGAGGAGAGACATTAGAAAATG 443  
 QY 121 AATTGATGCTTCTTAAAGATGGGACAGAAAACAGATCCTGTGTGATATTATTATTTG 180  
 Db 442 AATTGATGCTTCTTAAAGATGGGACAGAAAACAGATCCTGTGTGATATTATTATTTG 383  
 QY 181 AACGGATTACAGATTGAATGAAGTCAACCAAGTGAAGCATTCACATGAGAGAAAC 240  
 Db 382 AACGGATTACAGATTGAATGAAGTCAACCAAGTGAAGCATTCACATGAGAGAAAC 324  
 QY 241 AGACGAGAAAATCTTGATGGCTTCAACAAGATCAAC 278  
 Db 323 AGACGAGAAAATCTTGATGGCTTCAACAAGATCAAC 286

RESULT 4  
 AAH93806/c  
 ID AAH93806 standard; cDNA; 812 BP.  
 XX  
 AC AAH93806;  
 XX  
 DT 04-OCT-2001 (first entry)  
 XX  
 DE Human prostate-specific cDNA sequence P710P #4.  
 XX  
 KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;  
 KW cytostatic; gene therapy; metastasis; ss.  
 OS Homo sapiens.  
 XX  
 PN WO200151633-A2.  
 PD  
 XX 19-JUL-2001.  
 PF  
 XX 16-JAN-2001; 2001WO-US01574.  
 XX  
 XX 14-JAN-2000; 2000US-0483672.  
 PR  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;  
 PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;  
 PI Wang A, Meagher MD;  
 XX  
 DR WPI; 2001-425873/45.  
 XX  
 PT New polynucleotide encoding a prostate-specific protein, for  
 PT diagnosing, monitoring and treating prostate cancer in a patient and  
 PT for use in vaccines -  
 XX  
 PS Claim 1; Page 385; 543pp; English.  
 XX  
 CC The present invention describes polynucleotide sequences (I) which encode  
 CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,  
 CC and can be used in vaccine production and gene therapy. (II), (III),  
 CC antibodies to (II), fusion proteins comprising (II), and isolated  
 CC T cells prepared using (I) or (II) are used treat cancer in a patient.  
 CC (I) and the antibodies are also used in the detection of cancer in a  
 CC patient. The cancer that is diagnosed or treated is particularly  
 CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or  
 CC (I) can be used for monitoring the progression of cancer in a patient.  
 CC (I) and (II) can also be used to improve diagnostic and therapeutic  
 CC methods for prostate cancer. They can indicate the level of metastasis  
 CC as well as the prostate volume. AAH93357 to AAH93944 and AMO1115 to  
 CC AMO1318 represent polynucleotide and amino acid sequences used in the  
 CC exemplification of the present invention.  
 CC  
 XX Sequence 812 BP; 198 A; 189 C; 169 G; 256 T; 0 other;  
 SQ  
 Query Match 95.7%; Score 266; DB 22; Length 812;  
 Best Local Similarity 99.6%; Pred. No. 4.7e-76;  
 Matches 277; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 XX  
 QY 1 CAGGAACACAAAAGAGACACAGATCCCTGGAGAAATGCCCGCCGATCTTGGG 60  
 Db 562 CAGGAACACAAAAGAGACACAGATCCCTGGAGAAATGCCCGCCGATCTTGGG 503  
 QY 61 TCATCGATGAGCCTCGCCCTGTGCTGCTCCGCTTGTGAGGAGAGACATTAGAAAATG 120  
 Db 502 TCATCGATGAGCCTCGCCCTGTGCTGCTCCGCTTGTGAGGAGAGACATTAGAAAATG 443  
 QY 121 AATTGATGCTTCTTAAAGATGGGACAGAAAACAGATCCTGTGTGATATTATTATTTG 180  
 Db 442 AATTGATGCTTCTTAAAGATGGGACAGAAAACAGATCCTGTGTGATATTATTATTTG 383  
 QY 181 AACGGATTACAGATTGAATGAAGTCAACCAAGTGAAGCATTCACATGAGAGAAAC 240













